



FIG. 1A

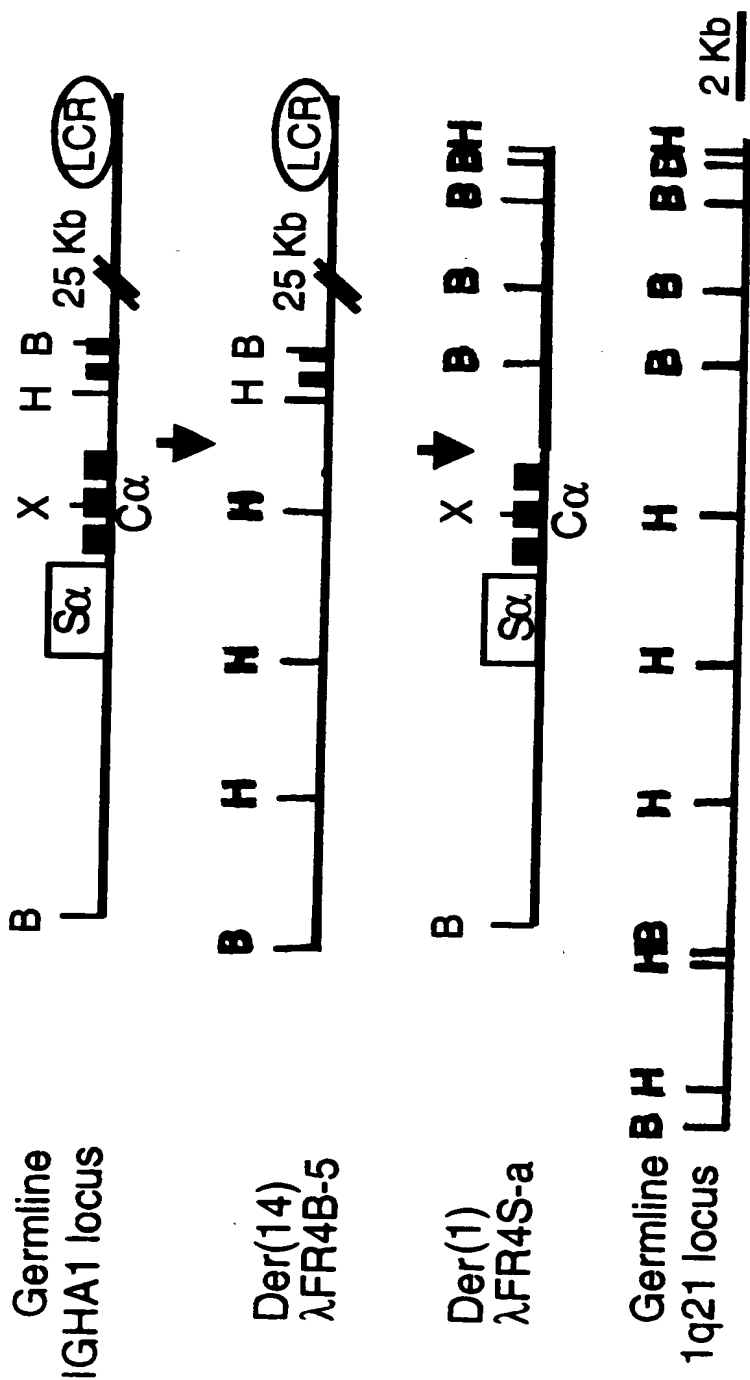


FIG. 1B

Chr 1 GGGCCTGACAGCAACTTTTCTTCTACTACTAGTTTCATCTTAAC
|||||
der14 GGGCCTGACAGCAACTTTTCTTCTACTACTAGTTTCATCTTAAC
Chr 14 TCCCCTGACGCATGCAGGAAGGGCACCTCCCCCTTAACC

FIG. 1BA

TTTATCCTGGTAACTGGCGGAGACAACCTGTCTTAAGTAACTGAAGGAAA
ACACTGCTCTGTACGGGGCACGTTGGGCACAGGTGCACACTCACA
|||||
ACACTGCTCTGTACGGGGCACGTTGGGCACAGGTGCACACTCACA

FIGURE 2A

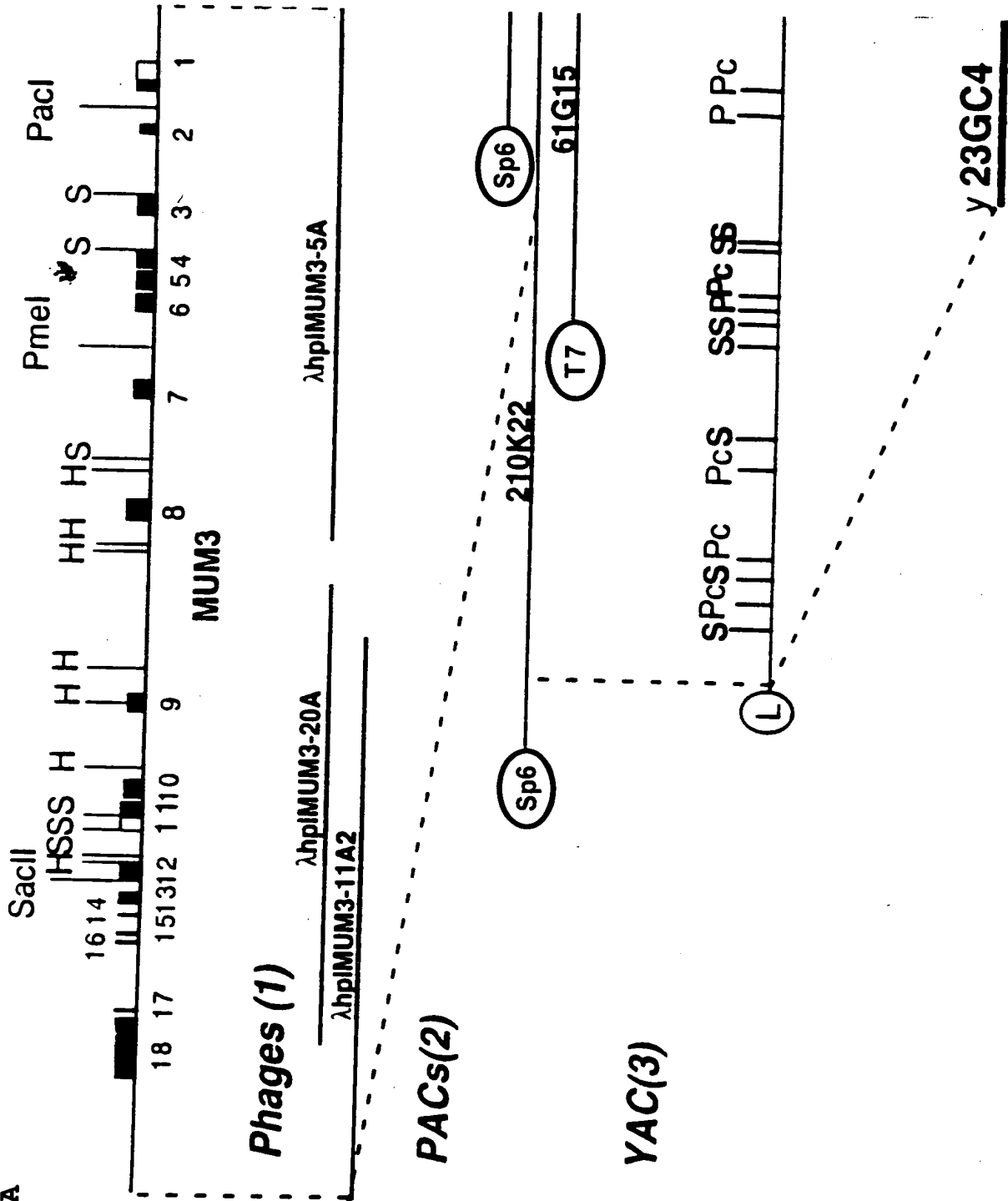


FIGURE 2AA

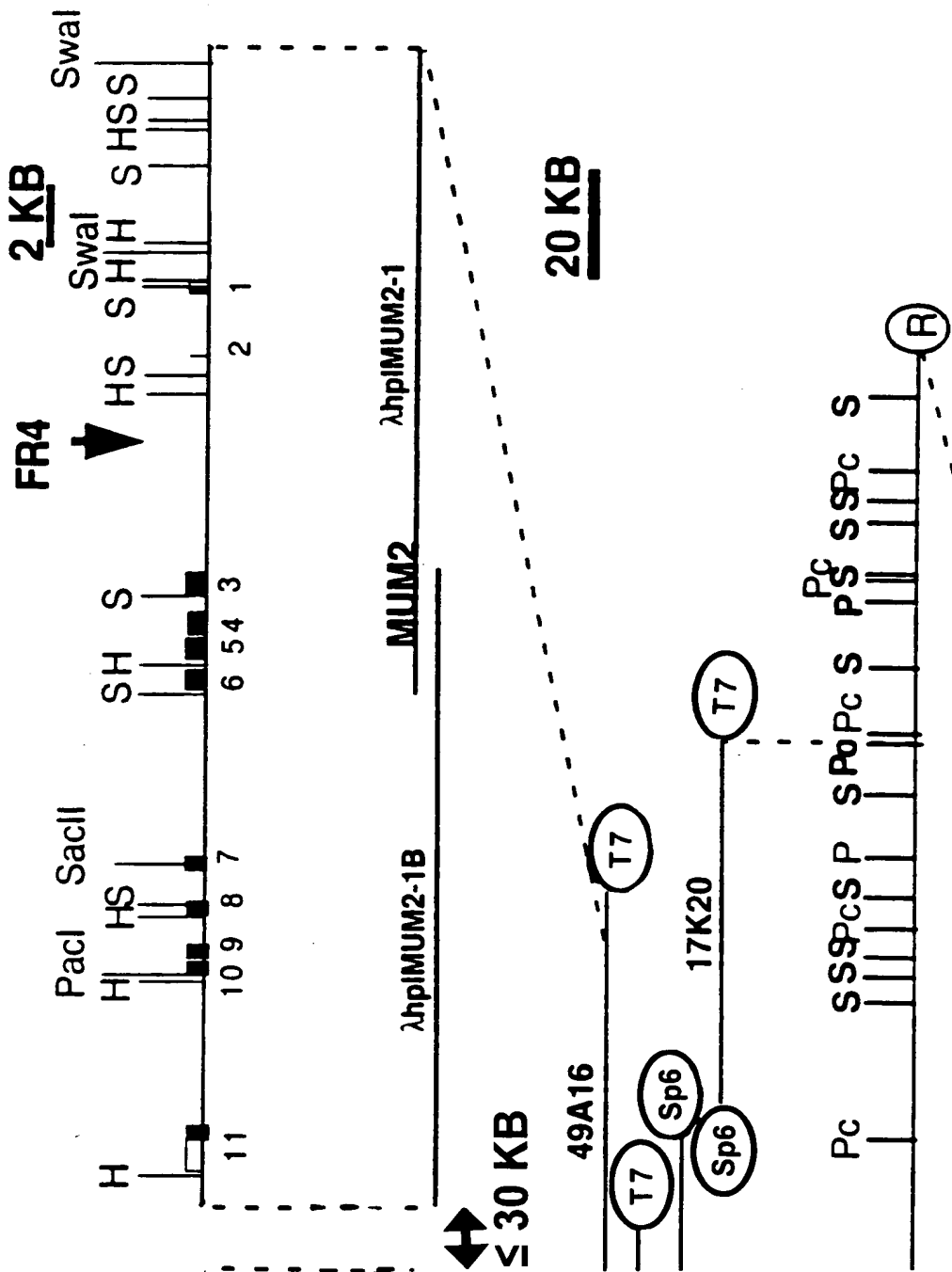
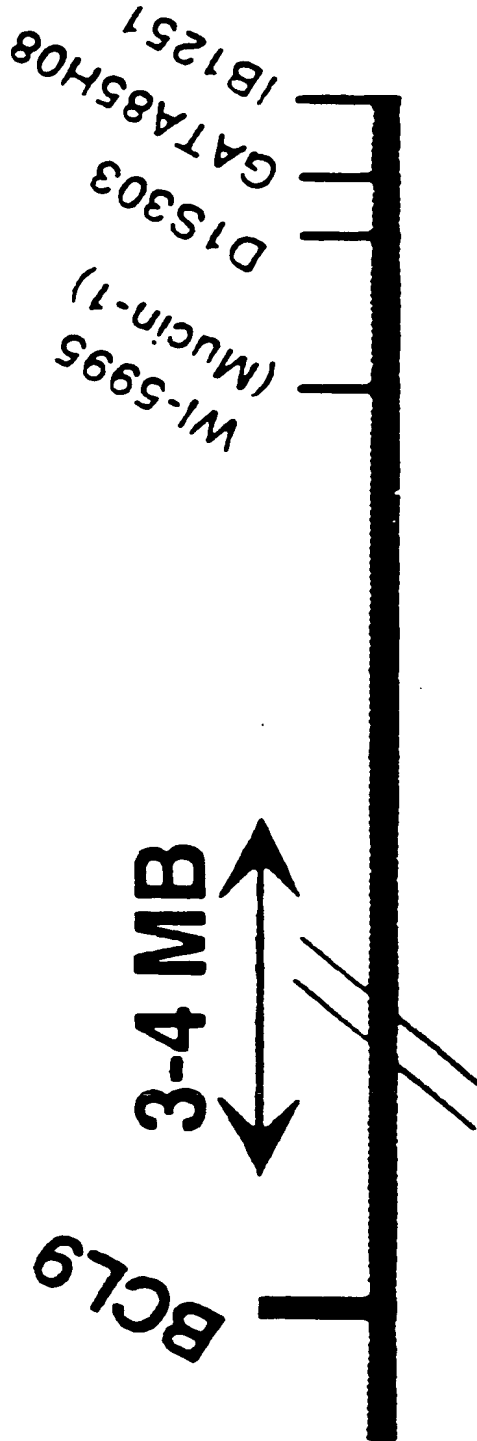


FIGURE 2B

CEN



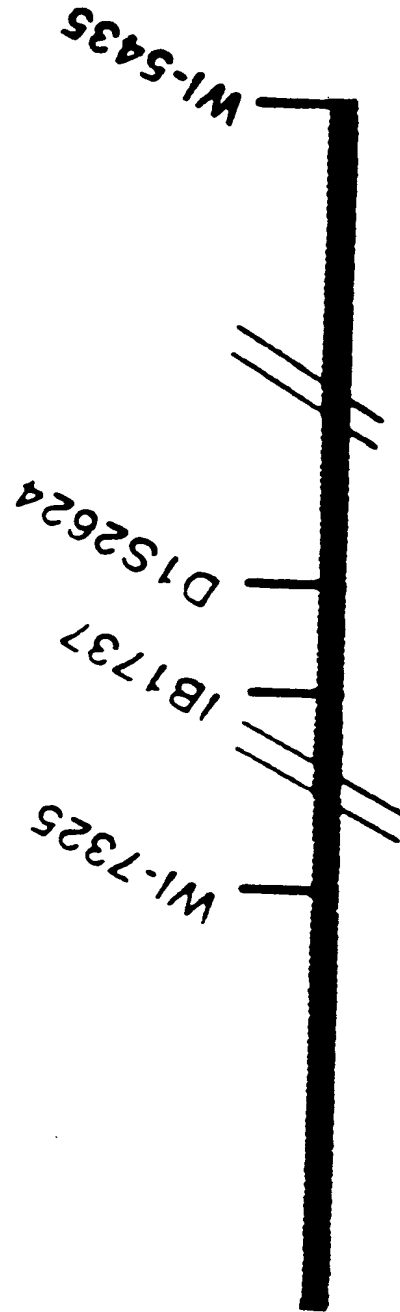


FIGURE 2BA

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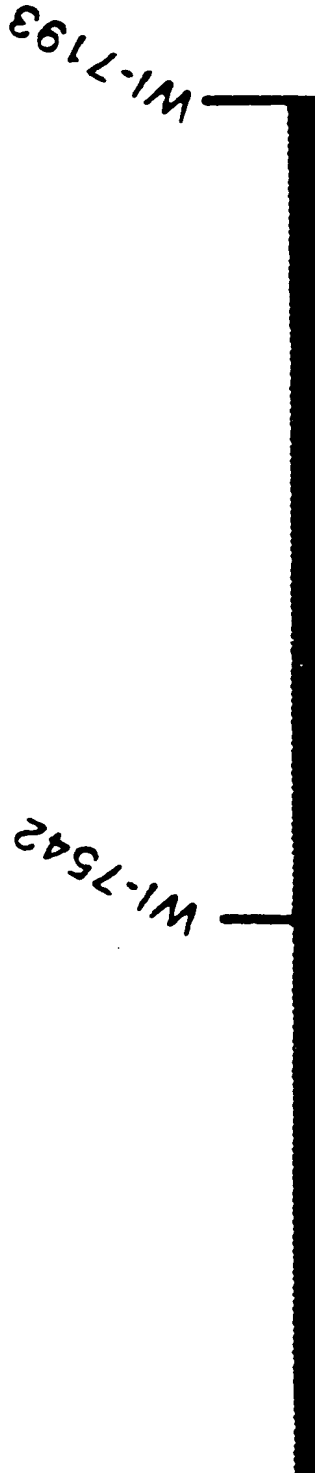


FIGURE 2BB

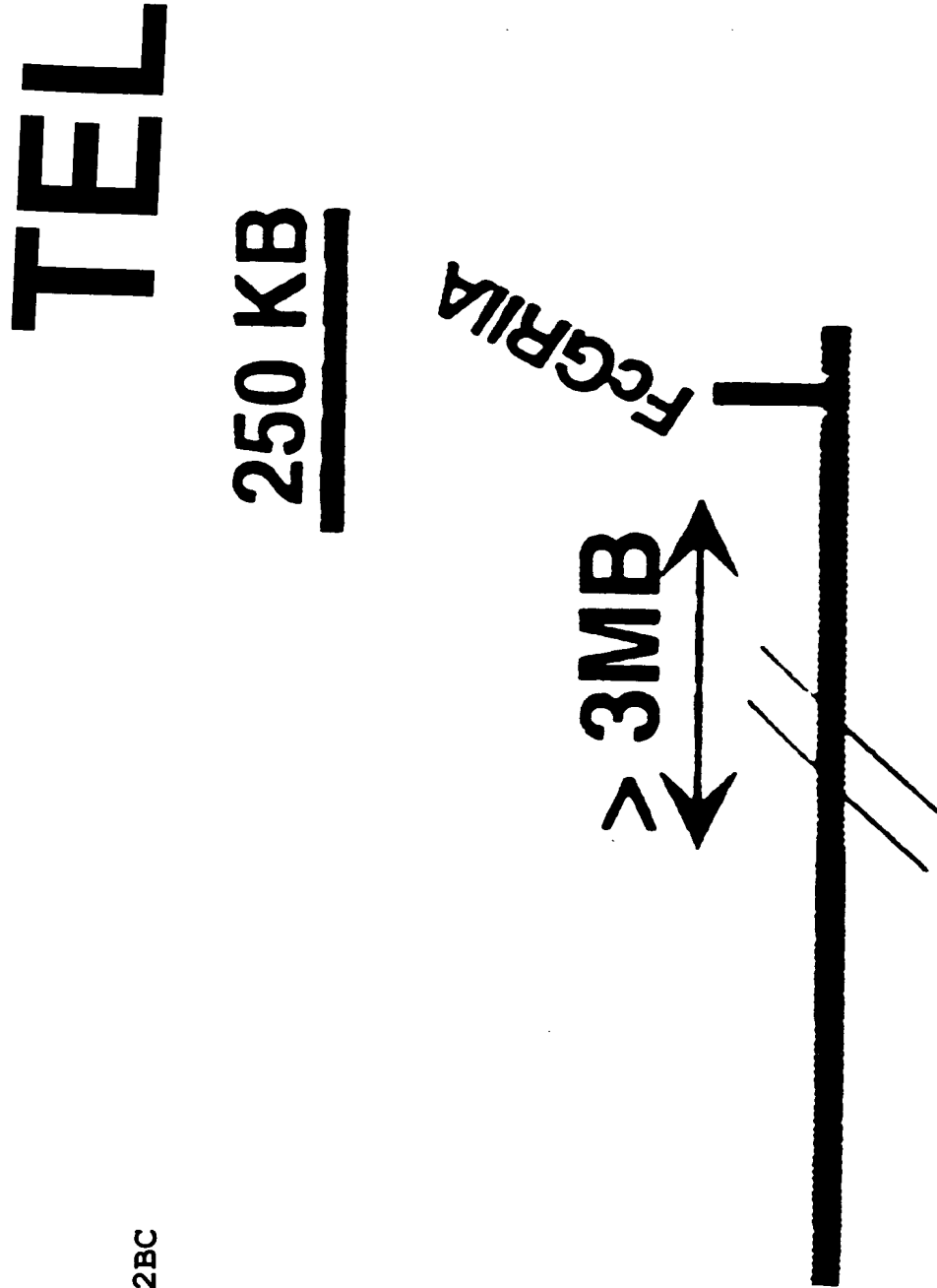
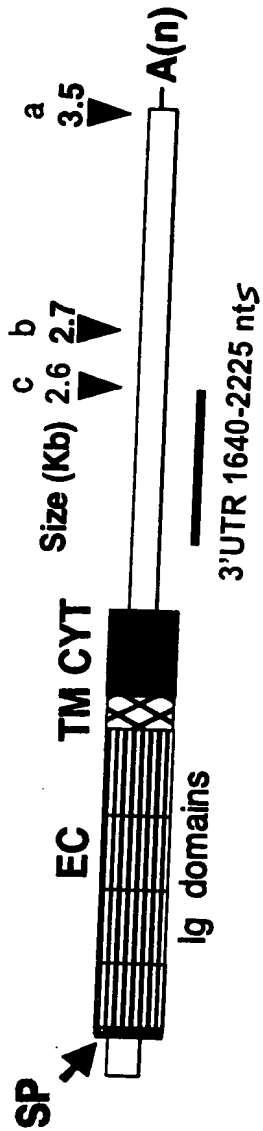


FIGURE 2BC

FIG. 3A



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FIG. 3B

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FIG. 3C

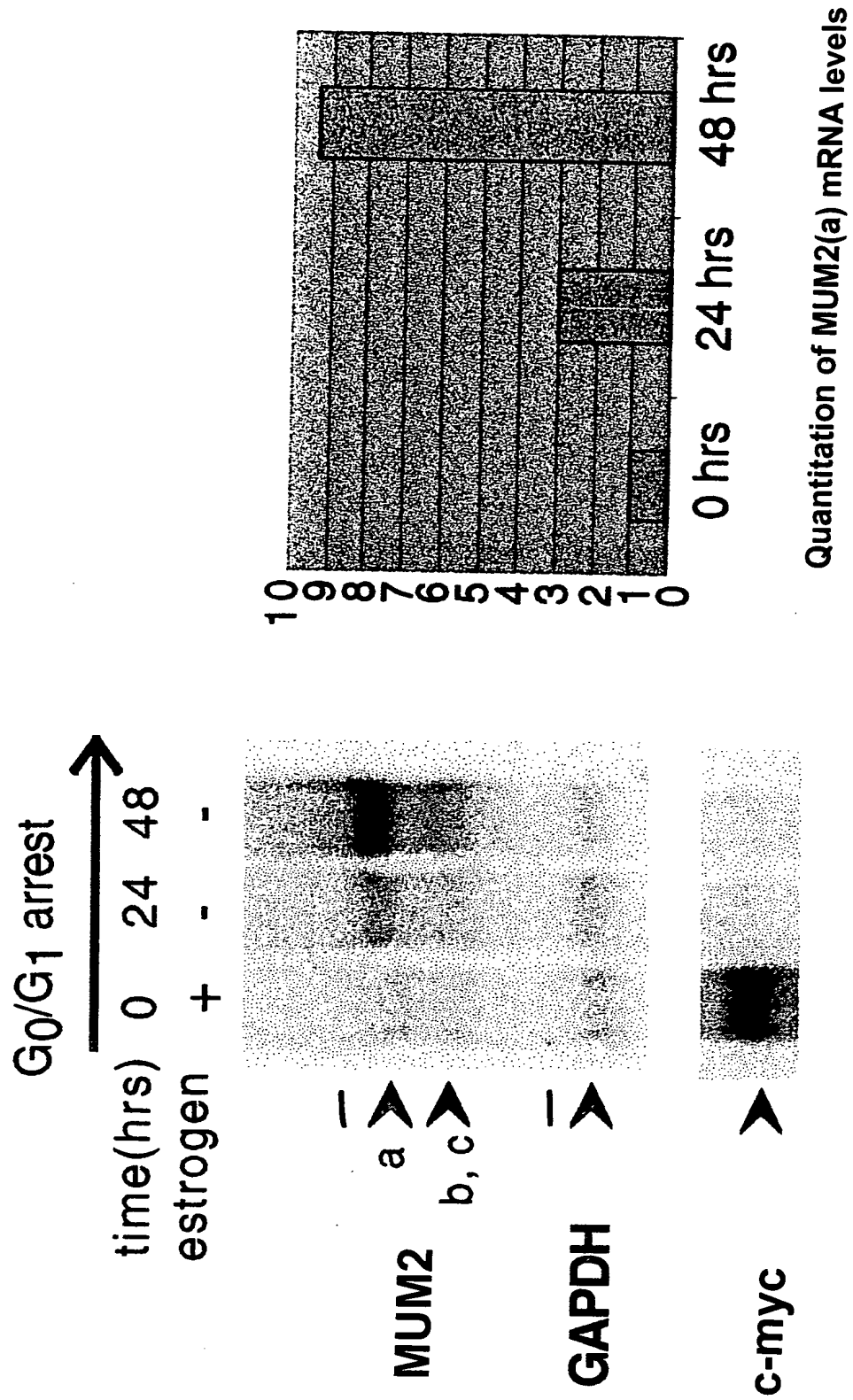


FIG. 4A

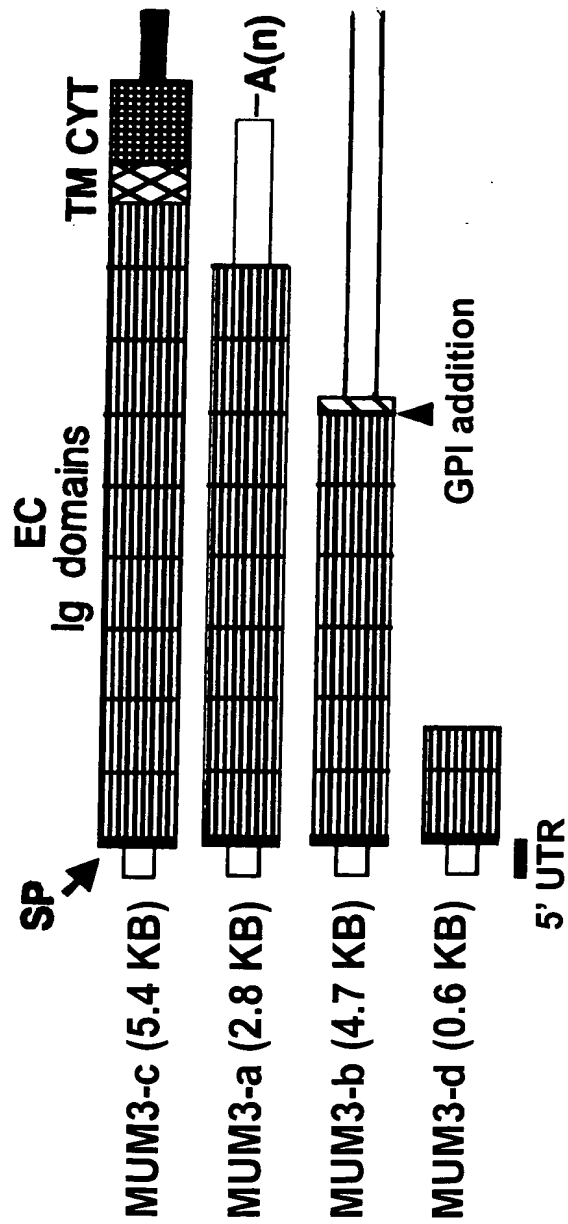
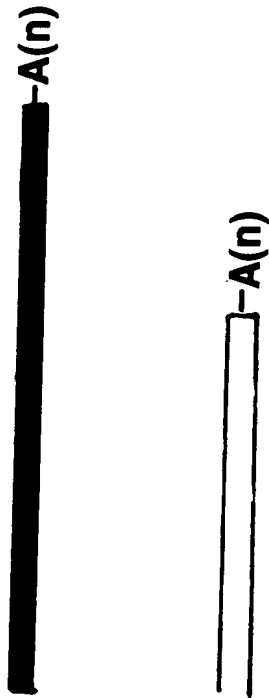
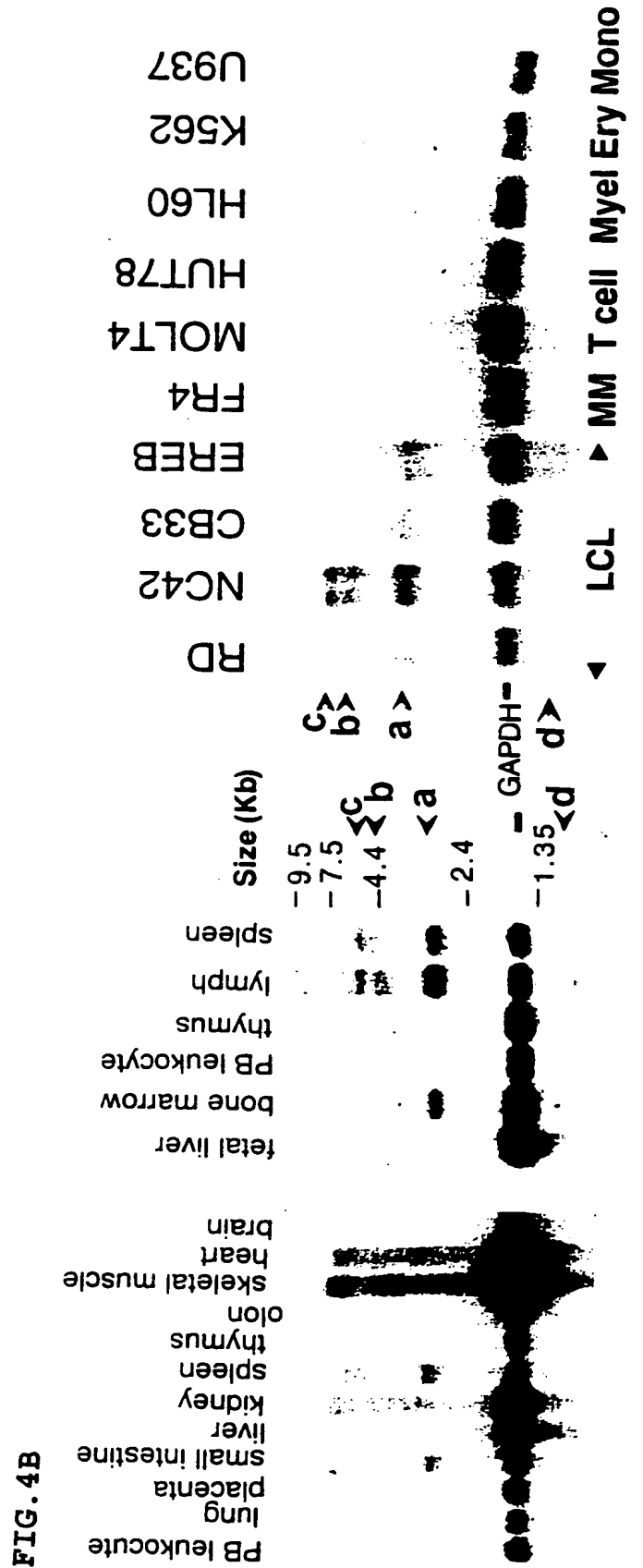


FIG. 4AA



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FIGURE 5

1 CTCAATCAGCTTTATGCAGAGAAGAGCTTACTGAGCTCACTGCTGGTGGTGGTAGGCAAGTGTCTTTGGCAA
78 TCTGGGCTGACCTGGCTTGTCTCTCAGAACTCCTTCTCAACCTGGAGCAGGCTTCCATGCTGTGGCGTCC
155 L L A F A P V C G Q S A A A H K P V I S V H P P W T 32
T T G T G G C C T T T G T C C A G T C T G T G G A C A A T C T G C A G T G C A C A C A A C C T G T G A T T C C G T C C A T C C T C C A T G G A C
232 T F F K G E R V T L T C N G F Q F Y A T E K T T W Y 58
C A C A T T C T T C A A G G A G A G A G T G A C T G A C T T G C A T G G A T T T C A G T T C T A T G C A C A G A G A A A C A C A T G G T
309 H R H Y W G E K L T L T P G N T L E V R E S G L Y 83
A T C A T C G G C A C T A C T G G G G A G A A A G T T G A C C C T G A C C C A G G A A A C A C C C T C G A G G T T C G G A A T C T G G A C T G T A C
386 R C Q A R G S P R S N P V R L L F S S D S L I L Q A 109
A G A T G C C A G G C C G G G C T C C C C A C G A A G T A A C C C T G T G C G T T G C T C T T T T C T T C A G A C T C C T T A A T C C T G C A G G C
463 P Y S V F E G D T L V L R C H R R K E K L T A V K 135
A C C A T A T T C T G T G T T G A A G G T G A C A C A T T G T T C T G A G A T G C C A G A A G A A G A A A T T G A C T G C T G T G A
540 Y T W N G N I L S I S N K S W D L L I P Q A S S N 160
A A T A C T T G G A A T T C T T T C C A T T T C T A A A A G C T G G A T C T T C T A T C C C A C A A G C A A G T T C A A A T
617 N N G N Y R C I G Y G D E N D V F R S N F K I K I 186
A A C A T G G C A A T T A T C G A T G C A T T G G A T G A G A T G A T G A T T A T T A G A T C A A A T T T C A A A A T A A T T A A A A T
694 Q E L F P H P E L K A T D S Q P T E G N S V N L S C 212
T C A A G A A C T A T T T C C A C A T C C A G A G C T G A A G C T A C A G A C T C T C A G C C T A C A G A G G G A A T T C T G T A A C C T G A G C T
771 E T Q L P P E R S D T P L H F N F F R D G E V I L 237
G T G A A C A C A G C T T C C T C C A G A G C G G T C A G A C A C C C C A C T T C A C T T C A A C T T C T T C A G A G A T G G C G A G G T C A T C C T G
848 S D W S T Y P E L Q L P T V W R E N S G S Y W C G A 263
T C A G A C T G G A G C A C G T A C C G G A C T C C A G C T C C A A C C G T C T G G A G A G A A A A C T C A G G A T C C T A T T G T G T G T G C
925 E T V R G N I H K H S P S L Q I H V Q R I P V S G V 289
T G A A A C A G T G A G G G T A A C A T C C A C A A G C A C A G T C C C T G C T A C A G A T C C A T G T G C A G C G G A T C C C T G T G T C G G G
1002 L L E T Q P S G G Q A V E G E M L V L V C S V A E 314
T G C T C T G G A G A C C C A G C C C T C A G G G G C C A G G C T G T T G A A G G G A G A T G C T G T G C T C T T G T C T G C T C C G T G G C T G A A
1079 G T G D T T F S W H R E D M Q E S L G R K T Q R S L 340
G G C A C A G G G A T A C C A C A T T C T C T G G C A C C G A G A G A C A T G C A G G A G A G T C T G G G A G G A A A C T C A G C G T T C C C T
1156 R A E L E L P A I R Q S H A G G Y Y C T A D N S Y G 366
G A G A C A G A G C T G G A G C T C C C T G C C A T C A G A C A G A C C C A T G C A G G G G A T A C T A C T G T A C A G C A G A C A C A G C T A C G
P V Q S M V L N V T V R E T P G N R D G L V A A G 391

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FIGURE 5A

1233 GCCCTGTCCAGAGCATGGTGTGAATGTCACTGTGAGAGAGACCCAGGCAACAGAGATGGCCTTGTCGCCCGGGGA
 1310 A T G G L L S A L L L A V A L L F H C W R R R K S G 417
 GCCACTGGAGGGCTGCTCAGTGTCTTCTCTGGCTGTGGCCCTGCTGTCTCACTGTGGCTGGAGGAGTCAGG
 1387 V G F L G D E T R L P P A P G P G E S S H S I C P A 443
 AGTTGGTTTCTTGGGAGACGAACCCAGGCTCCCTCCGCTCCAGGCCCCAGGAGAGTCTCCCATTCCTGCCCCTG
 Q V E L Q S L Y V D V H P K K G D L V X S E I Q T 468
 1464 CCCAGGTGGAGCTTCAGTGTGTGTATGTGTATGATGTACACCCCAAAAGGGAGATTGTTGTATCTCTGAGATCCAGACT
 T Q L G E E E A N T S R T L L E D K D V S V Y S 494
 1541 ACTCAGCTGGGAGAGAGAGGAAGCTAATACCTCCAGGACACTTCTAGAGGATAAGGATGTCTCAGTTGTCTACTC
 E V K T Q H P D N S A G K I S S K D E S * 515
 1618 TGAGGTAAAGACACACACCCAGATAACTCAGCTGGAAGATCAGCTCTAAGGATGAAGAAAGTTAAGAGAAATGAAA
 1695 AGTTACGGGAACGTCCTACTCATGTGATTTCTCCCTTGTCCAAAGTCCAGGCCAGTGCAGTCTTGGGGCACCTG
 1772 GAATGATCAACTCATTCAGCTTTCTAAATCTCTCATGCATATGCATTCACTCCAGGAATACTCATTCGTCTACT
 1849 CTGATGTTGGGATGGAATGGCTCTGAAAGACTTCACATAAATGACCAGGATCCACAGTTAAGAGAAAGACCCCTGTAG
 1926 TATTTGCTGTGGGCTGACCTAATGCATTCCTTAGGCTGTCTTGTAGAGAGGGGATGAAGAGAGAGAGAGGACTGT
 2003 TATGAAAAACAGAACACAAATTTTGGTGAAATTTGGGATTTGCAGAGATGAAAAGACTGGGTGACCTGGATCTCTGC
 2080 TTAATACATCTACAACTTGTCTCACTGGAGACTCACTTGCATCAGTTTGTAACTGTGAGTGGCTGCACAGGCA
 2157 CTGTGCAACAATGAAAAGCCCTTCACTTCTGCTGCACAGCTTACACTGTCAAGGATTCAGTTGCAGATTAAAGAA
 2234 CCCATCTGGAATGTTTACAGAGAGAGGAATTTAAAGAGGACATCAGAAGAGCTGGAGATGCAAGCTCTAGGCTGC
 2311 GCTTCCAAAGCAAAATGATAATTAATGTTAATGTATTAGTGACAAAGATTTGCCAACATTAGAGAAAGAGACACAAA
 2388 TATAAAATTAAAAAATTAAAGTACCAACTCTCCAAAACCTAAATTTGAACTTAAATATTAGTATAAAGTCAATAATAA
 2465 CTCTGCCTTTAAATAAAAAAATAAAAAA

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FIGURE 6a

1 CCGTGCAGTGTCTGACTGTAGATCAAGTCCAAACCTGTTTGGAAATTGAGGAAACTTCTCTTTTGATCTCAGCCCTTG
 81 GTGGTCCAGGCTTCAATGCTGTGGGTGATATTACTGGTCTGGCTCCTGTCTAGTGGACAGTTTGCAGGACACCCAG
 161 GCCCATTTTCTCCAGCCTCCATGGACCACAGTCTTCCAGGAGAGAGAGTGTACCCCTCACTTGAAGGGATTTCGCT
 241 TCTACTCACCACAGAAACAATGGTACCATCGGTACCTTGGGAAAGAAATACTAAGAGAAACCCAGACAATATCCTT
 321 GAGGTTCAGGAATCTGGAGAGTACAGATGCCAGGCCAGGCTCCCTCTCAGTAGCCCTGTGCACCTTGGATTTCCTTC
 401 AGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGACTCTGTGGTCTGAGGTGCCGGCAAGCGGAAG
 481 TAACACTGAATAATACTATTACAAGAATGATAATGTCTGGCATTCCTTAATAAAGAACTGACTTCCATATTCCTCAT
 561 GCATGTCTCAAGGACAAATGGTGCATATCGTGTACTGGATATAAGGAAGTTGTTGCCCTGTTTCTTCCAATACAGTCAA
 641 AATCCAAGTCCAAGAGCCATTTACACGTCAGTGTGAGAGCCAGCTCTTCCAGCCCATCAGCGGGAACCCAGTGACCC
 721 TGACCTGTGAGACCCAGCTCTCTTAGAGAGGTCAGATGTCCCGCTCCGGTTCCTTCCAGAGATGACCAGACCCCTG
 801 GGATTAGGCTGGAGTCTCTCCCGAATTTCCAGATTACTGCCATGTGGAGTAAAGATTTCAGGGTTCTACTGGTGTAAAGGC
 881 AGCAACAATGCCTCACAGCGTCATATCTGACAGCCCGAGATCCTGGATACAGGTGCAGATCCCTGCATCTCATCTGTCC
 961 TCACCTCAGCCCTGAAAGGCTCTGAATTTGAGGGAACCAAGGTGACACTTCACTGTGAACCCAGGAAGATTCTCTG
 1041 CGCACTTTGTACAGGTTTATCATGAGGGTGTCCCTCCCTGAGGCACAAAGTCAGTCCGCTGTGAAGGGGAGCATCCATCAG
 1121 CTTCTCACTGACTACAGAGAATTCAGGGAATCTACTGACAGCTGACAAATGGCCCTGGGCCAAGCCAGTAAGGCTG
 1201 TGAGCCTCTCAGTCACTGTTCCTGCTCATCTCTCAACCTCAGCTCTCCTGAGGACCTGATTTTGGAGGGAGCC
 K V T L H C E A Q R G S L P I L Y Q F H H E D A A L E 422

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FIGURE 6aA

1281 AAGGTGACACTTCACTGTGAAGCCACAGAGAGGTTTCACTCCCATCTCTGTACCAGTTTCATCATGAGGATGCTGCCCTGGA
 R R S A N S A G G V A I S F S L T A E H S G N Y Y C T449
 1361 GCGTAGTGGCCAACTCTGCAGGAGGAGTGGCCATCAGCTTCTCTGACTGCAGAGCATTCAGGGAATCTACTACTGCA
 A D N G F G P Q R S K A V S L S I T V P V S H P V L 475
 1441 CAGCTGACAATGGCTTTGGCCCCCAGCGCAGTAAGCGGTGAGCCTCTCCATCAGTGTCCCTGTGTCTCATCTCTGTCTC
 T L S S A E A L T F E G A T V T L H C E V Q R G S P Q 502
 1521 ACCCTCAGCTCTGCTGAGGCCCTGACTTTTGAAGGAGCCACTGTGACACTTCACTGTGAAGTCCAGAGAGGTTCCCCACA
 I L Y Q F Y H E D M P L W S S T P S V G R V S F S F529
 1601 AATCCTATACCAGTTTATCATGAGGACATGCCCTGTGGAGCAGCTCAACACCTCTGTGGGAAGAGTGTCTCTCAGCT
 S L T E G H S G N Y Y C T A D N G F G P Q R S E V V 555
 1681 TCTCTGACTGAAGGACATTCAGGGAATTAATACTACTGCACAGCTGACAATGGCTTTGGTCCCGCAGCGCAGTGAAGTGGTG
 S L F V T V P V S R P I L T L R V P R A Q A V V G D L 582
 1761 AGCCTTTTGTCACTGTTCCAGTGTCTCGCCCCCATCTCACCTCAGGGTTCCCGAGGCCAGGCTGTGGTGGGGACCT
 L E L H C E A P R G S P P I L Y W F Y H E D V T L G S 609
 1841 GCTGGAGCTTCACTGTGAGGCCCGCAGAGGCTCTCCCCAATCTGTACTGGTTTATCATGAGGATGTACCCCTGGGA
 S S A P S G G E A S F N L S L T A E H S G N Y S C E 635
 1921 GCAGCTCAGCCCCCTCTGGAGGAGAAGCTTCTTTCAACCTCTCTGACTGCAGAACATTTCTGGAACTACTCATGTGAG
 A N N G L V A Q H S D T I S L S V I V P V S R P I L T 662
 2001 GCCAACAAATGGCTAGTGGCCCGCAGCAGTGACACAATATCACTCAGTGTATAGTTCCAGTATCTCGTCCCATCTCAC
 F R A P R A Q A V V G D L L E L H C E A L R G S S P I689
 2081 CTTCAGGGCTCCCAGGGCCAGGCTGTGGTGGGGACCTGCTGGAGCTTCACTGTGAGGCCCTGAGAGGCTCCTCCCCAA
 L Y W F Y H E D V T L G K I S A P S G G G A S F N L 715
 2161 TCCTGTACTGGTTTATCATGAAGATGTCACCTGGTAAGATCTCAGCCCCCTCTGGAGGAGGGCCCTCCTTCAACCTC
 S L T T E H S G I Y S C E A D N G L E A Q R S E M V T 742
 2241 TCTCTGACTACAGAACATTTCTGGAATCTACTCCTGTGAGGCAGACAATGGTCTGGAGGCCCGCAGCGCAGTGAGATGGTGAC
 L K V A G E W A L P T S S T S E N * 759
 2321 ACTGAAAGTTGCAGGTGAGTGGGCCCTGCCACAGCAGCAGCATCTGAGAACTGACTGTGCTTCTCCCTGCAGCTGA
 2401 AATGGAGCCACAGAGCTCCTCAGGGCTGTTGCTGTGTGGCATCCAGCACACTTCTCTGCTGCAGAACCTCCCTGTG
 2481 AAAGTCTCGGATCCTTTGTGGTATGGTTCCAGGAATCTGATGTTTCCAGCAGTCTTCTTGAAGATGATCAAGCACCTC
 2561 ACTAAAATGCAATAAGACTTTTGTAGAACATAAATACTATATCTGAAGTGAATATTATACATGAAATGAAACCAAGA
 2641 ATTCTGAGCATATGTTTCTGCGGTAGAAAGGATTAAGCTGTTTCTTGTCCGGATTCTTCTCTCATTTGACTTCTAAGAA
 2721 GCCTCTACTCTTGAGTCTCTTTTCATTACTGGGATGTAAATGTTTCTCTTACATTTCCACATTAAAAATCCTATGTTAACGA
 AAAA

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FIGURE 6b

1 CGGTGCAGTCTCCTGACTGTAAGATCAAGTCCAAACCTGTTTGGAAATTGAGGAAACTTCTCTTTTGATCTCAGCCCTTG
22 M L L W V I L L V L A P V S G Q F A R T P R
81 GTGGTCCAGGTCTTCATGCTGCTGGTGATATTAATGCTGCTGGCTCCTGTGACGTGGACAGTTTGCAAGGACACCCCG
49 P I I F L Q P P W T T V F Q G E R V T L T C K G F R F
161 GCCCATTTATTTCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGAACCTCCTCACTTGCAAGGATTTTCGCT
75 Y S P Q K T K W Y H R Y L G K E I L R E T P D N I L
241 TCTACTCACAGAAACAAATGTTACCATCGGTACCTTGGGAAAGAAATACTAAGAGAAACCCACAGACAATATCCTT
102 E V Q E S G E Y R C Q A Q G S P L S S P V H L D F S S
321 GAGGTTCAGGAATCTGGAGAGTACAGATGCCAGGCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTTGGATTTTCTTC
129 A S L I L Q A P L S V F E G D S V V L R C R A K A E V
401 AGCTTCGCTGATCCTCAAGCTCCACTTTCTGTGTTTGAAGGAGACTCTGTGTTCTGAGGTGCCGGGCAAGGCGGAAG
155 T L N N T I Y K N D N V L A F L N K R T D F H I P H
481 TAACACTGAATAATACTATTACAAGAAATGATAATGCTCTGGCATTCTTAATAAAGAACTGACTTCCATATTCCTCAT
182 A C L K D N G A Y R C T G Y K E S C C P V S S N T V K
561 GCATGTCTCAAGGACAATGGTGATATCGCTGTACTGGATATAAGGAAAGTTGTGCCCTGTTTCTTCCAATACAGTCAA
209 I Q V Q E P F T R P V L R A S S F Q P I S G N P V T L
641 AATCCAAGTCCAAGAGCCATTTACAGTCCAGTGTGAGAGCCAGCTCCTCCAGCCCATCAGCGGGAACCCAGTGACCC
235 T C E T Q L S L E R S D V P L R F R F R D D Q T L
721 TGACCTGTGAGACCCAGCTCTCTCTAGAGAGGTCAGATGTCCCGTCCGGTTCCTTCCAGAGATGACCAACCCCTG
262 G L G W S L S P N F Q I T A M W S K D S G F Y W C K A
801 GGATTAGGCTGGAGTCTCTCCCGAATTTCCAGATTAATGCCATGTGGAGTAAAGATTCAGGGTTCTACTGGTGAAGGC
289 A T M P H S V I S D S P R S W I Q V Q I P A S H P V L
881 AGCAACAATGCCCTCACAGCGTCATATCTGACAGCCCGAGATCCTGGATACAGGTGCAGATCCCTGCATCTCATCTGTCC
315 T L S P E K A L N F E G T K V T L H C E T Q E D S L
961 TCACCTCAGCCCTGAAAAGGCTCTGAATTTTGAGGGAACCAAGGTGACACTTCACTGTGAAACCCAGGAAGATTCTCTG
342 R T L Y R F Y H E G V P L R H K S V R C E R G A S I S
1041 CGCACTTTGTACAGGTTTATCATGAGGGTGTCCCTGAGGCACAGTCACTCGCTGTGAAAGGGAGCATCCATCAG
369 F S L T T E N S G N Y Y C T A D N G L G A K P S K A V
1121 CTTCTCACTGACTACAGAGAATTCAGGGAACCTACTACTGCACAGCTGACAATGGCCTTGGCCCAAGCCAGTAAGGCTG
395 S L S V T V P V S H P V L N L S S P E D L I F E G A
1201 TGAGCCTCTCAGTCACTGTTCCCGTGTCTCATCTCTCAACCTCAGCTCTCTGAGGACCTGATTTTGTAGGGAGCC
422 K V T L H C E A Q R G S L P I L Y Q F H H E D A A L E
1281 AAGTGACACTTCACTGTGAAGCCAGAGAGGTTCACTCCCATCTCTGTACCAGTTTTCATCATGAGGATGCTGCTCCCTGGA

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FIGURE 6bA

R R S A N S A G G V A I S F S L T A E H S G N Y Y C T 449
1361 GCGTAGGTCGGCCAACTCTGCAGGAGGAGTGCCCATCAGCTTCTCTGACTGCAGAGCATTCAGGGAACACTACTACTGCA
A D N G F G P Q R S K A V S L S I T V P V S H P V L 475
1441 CAGCTGACAAATGGCTTTGGCCCCCAGCGCAGTAAGGCGTGAGCCTCTCCATCAGCTGTCCTGTCTCATCTCCTGTCTC
T L S S A E A L T F E G A T V T L H C E V Q R G S P Q 502
1521 ACCCTCAGCTCTGCTGAGGCCCTGACTTTTGAAGGAGCCACTGTGACACTTCACTGTGAAGTCCAGAGAGGTTCCCCACA
I L Y Q F Y H E D M P L W S S S T P S V G R V S F S F 529
1601 AATCCTATACCAGTTTATCATGAGGACATGCCCTGTGGAGCAGCTCAACACCCCTCTGTGGGAAGAGTGTCTTCAAGCT
S L T E G H S G N Y Y C T A D N G F G P Q R S E V V 555
1681 TCTCTGACTGAAGGACATTCAGGGAATTACTACTGCACAGCTGACAAATGGCTTTGGTCCCGCCAGCGCAGTGAAGTGGTG
S L F V T G K C W V L A S H P P L A E F S L T H S F K 582
1761 AGCCTTTTGTCACTGGTAAGTGTGGTCTTGGCCAGTCACCCACCCCTGGCTGAGTCTCTCTCACCCATTCTCTTTAA
N L F A L S S F L P . stop 592
1841 AAATCTGTTGCACTGTCCAGTTTCTCTCCCTTAATCAACTTAATCCCTTCTTGGCTTCTCTCAACTAAGCTGGG
1921 GTTTTCGTAATAAGTCTGGCTCAGCCAGACCCCTAAACAGCTCAGTAGATTCCCGAGCTTTTACCAATGAATT
2001 TATTTATGTATTTCTCTCTCATTCCTGTATGTTCACAGTACGCCAAATTTTCTGTGATGACGGAGCGTGTCTACT
2081 TCTCTACTGACATTTACATATTAACTTAGCTACAGCACAGTCTTATAGATAAATATGGTCAAGACCTTAATTTCTCCA
2161 AAGGATTTCCAAATCTTATGTAGATTTGGAGAAAGCTGTGGTAACAAGGGGGAATGGCTCCCTAGGAACCAACTCC
2241 TCAACTTCTGGAGTTTATGATCCCTGTTTCTAACCTGCTAAATCAGTATCATTTTATTTATTTTAAATAA
2321 ACTATTGTTGAAGTATGACATACATTCAAGAAACGTTGCAAAATGTATGTGTACGATTTGGTGTCTTTTAGGAGCTAA
2401 GTTGCTTCTGTTTACTTGAATCTTTGTTTATAGAAACTGGGGGAAAGTTTACTTCTTTTTCAGAGAAGCCAAATGGTA
2481 TGATAGAAAATCTTTGAGCCTGATGTGTGACACATGCCCCCTAGCATAACTTTGTTGAGTAAAGAGGTTATTTTAAATGT
2561 GAATGTTCTGAGACTACTCCAAGTCAGAGCCAAATCTACTAGGAAGCTTCTAGACTTCACTCATTTCTGTCATCCCATTAC
2641 TATCTTTTATCCATGTTTACTTCTTCTCATATTTCAGCAGCATCTTAAGCCTCTTATTTTCTGTTCTTGACTGTCA
2721 CCTTAATGCCAGTAGAATGTAAAGCTTTCATGAGAACAGAACTGCATCCATCTTGGTCTTTCACAAACATCCCTGTGCTACT
2801 CAGTGTGTCACACAGTAGGTCCTCAGTCAACATTTGTAAATTTAGTGGACAGATGATATGACAAGATGATAGAGGGGA
2881 TTTAAATAATCATCTAGCAAGAGGCAAGGGAATAAACAAGCTATTTTAGAATAATGAATACCAATTTGAAGCAGTA
2961 AGAATAGATTGGATATCTTTGAAAACCATTAATTTGAATGAAGAACCAATTTGAGAAAACAATACAGAATGCAAGTAGAA
3041 AGATACAGAAATAAGGCAAAAGTTATAATATGGAATCAGACAAATGGATTTGTCTGTATCCAGTTATGTGGATAATTAA
3121 AATGGAGACCTCAGAAAATTGAACCGAAGAGTAAATGAACTCAAAATGTAGTAGAAATTTGTTGGGAAGTAAAGAAA
3201 ACTTGAATATGTAGATCAGAACATATATGTTGATGACGTTATTTGACTTTTGAGGTTAAAAATATATATATGTGCTATGAT
3281 TATGGGGAAAAAAGCAGTCGTCTCAGAAAGAAAAACATCAAGTTAGTCTTAGACTTTGCAAGTGCACACTCAGTACCAAGAG

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FIGURE 6bB

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3361 AGAGGAGGCCGAGACTTGGACCTGCGAGGGGAAGAAATAAACCAGAAAATTTTATATCAATTCAAAAAGACATTGTCAAAA
3441 TACAGGGATTTCAGGAAACTGAGAAATGCACCTAAGCCTTCTGGAAAAAACAACCTAATGACAAAAATCTAGCCCCAACAGATGT
3521 AAATGAATATAAAGGACTCATAATGAGGAAACCGCATTTATGACTGGCTCTCAACCTGGCCGCAATATTAGACTCGTCAAA
3601 GACCTTTGTAAAAGGTCACACATTGACTCGTCAAAAGCCCTCTCCAGACTAATTCAATTTCAGAAATCTCACAGATGGGGCC
3681 ACAGAAATCAGTATTTTGTGACACACACCTCAAGTGAGAAATATTGTGTAGACAAAGATTGGAAACCCACTGATTTAGATATAGA
3761 AACAAAGGCTAATCAACTGTGAGAAATTAATGGTCACAGAAATAGAAAGTAACTATTATGAACACTGAAATGTAAATAAAT
3841 GTAACAAAGAAATAATAGTTAGAGGAAGGAGAGGAAGTAAGGAACAATCATTTTCTCATGATTATTATTATTTTCAGAGTA
3921 AATTGTGAGTTATTTCACAAATTCAAAAAGAAATGGACTGTTTTTAAAAAATTAGTAATAGATTTCAAAAATGTCCATTTTGT
4001 AATCGTTTCTGAATACTTTGTCAACAGTTACTCATCTAATTAATGGCTTATACTTCACTAAAAATTCATGGAAAAACCACTA
4081 GTAGCCTGTAGAGTCACATAGGAGAGAACAAAGTGAATTTCTTTGGGTGGCGCAAGCATAGATGTTAGGACTGACAAAAAAA
4161 AATAATAAAAAATAAACCTGTGCAATTGATATGATCACAAATGATCAGGGAAGAGGAAACAGAAACTCTCATACGCCATTTA
4241 TTACAAGTGTAATTTGGTTCAACCTTTTCGTCTTAAATGACACATTTGTAATTGTATATATTTATGGAAGCACAGTTTGAT
4321 ATTTTGATATACATACATGGTATATAACGATCAAAATTAGGATATTTAATGTACCCCATCATCTCATGCAATTTATCATTTCT
4401 TTGGAATAAA AACATTCAA AGCCAAAAA AAAAAAAA AAAAAA
```

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FIGURE 6c-1

```
1  CGGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTTTGGAAATTGAGGAAACTTCTCTTTTGATCTCAGCCCTTG 22
      M L L W V I L L V L A P V S G Q F A R T P R
81  GTGGTCCAGGTCTTCATGCTGTGGTGATATTACTGGTCTGCTGCTGTGACGTGGACAGTTTGAAGGACACCCAG
      P I I F L Q P P W T T V F Q G E R V T L T C K G F R F
161  GCCCATTATTTTCTCCAGCCTCCATGGACCACAGTCTTCCCAAGGAGAGAGAGTGAACCTCAGCTTCAAGGGATTTCGCT
      Y S P Q K T K W Y H R Y L G K E I L R E T P D N I L
241  TCTACTCACCACAGAAACAATGTACCATCGGTACCTTGGGAAGAAATACTAAGAGAAACCCACAGACAATATCCTT
      E V Q E S G E Y R C Q A Q G S P L S S P V H L D F S S
321  GAGGTTCAGGAATCTGGAGGTACAGATGCCAGGCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTCCTTC
      A S L I L Q A P L S V F E G D S V V L R C R A K A E V
401  AGCTTCGCTGATCCTGCAAGCTCCACTTCTGTGTTTGAAGGAGACTCTGTGGTTCTGAGGTGCCGGGCAAGGGCGGAAG
      T L N N T I Y K N D N V L A F L N K R T D F H I P H
481  TAACACTGAATAATACTATTACAGAATGATAATGTCTGGCATTCCTTAATAAAGAACTGACTTCCATATTCCTCAT
      A C L K D N G A Y R C T G Y K E S C C P V S S N T V K
561  GCATGTCTCAAGGACAATGGTGCTATCGCTGTACTGGATATAAGGAAGTTGTTGCCCTGTCTTCTTCCAATACAGTCAA
      I Q V Q E P F T R P V L R A S S F Q P I S G N P V T L
641  AATCCAAGTCCAAGAGCCATTTACACGTCACAGTGTGAGAGCCAGCTCCTTCCAGCCCATCAGCGGGAACCCAGTGACCC
      T C E T Q L S L E R S D V P L R F R F R D D Q T L
721  TGACCTGTGAGACCCAGCTCTCTCTAGAGAGGTACAGATGTCCCGCTCCGGTTCCTTCCAGAGATGACACACCCCTG
      G L G W S L S P N F Q I T A M W S K D S G F Y W C K A
801  GGATTAGGCTGGAGTCTCTCCCGAATTTCCAGATTACTGCCATGTGGAGTAAGATTTCAGGGTTCTACTGGTGAAGGC
      A T M P H S V I S D S P R S W I Q V Q I P A S H P V L
581  AGCAACAATGCCTCACAGGTCATATCTGACAGCCCGAGATCCTGGATACAGGTGCAGATCCCTGCATCTCATCTGTCC
      T L S P E K A L N F E G T K V T L H C E T Q E D S L
961  TCACTCTCAGCCCTGAAAAGGCTCTGAATTTTGAAGGAACCAAGGTGACACTTCACTGTGAACCCAGGAAGATTCTCTG
      R T L Y R F Y H E G V P L R H K S V R C E R G A S I S
1041  CGCACTTTGTACAGGTTTATCATGAGGGTGTCCCCCTGAGGCACAAAGTCAGTCGCTGTGAAGGGAGCATCCATCAG
      F S L T T E N S G N Y Y C T A D N G L G A K P S K A V
1121  CTTCTCACTGACTACAGAGAATTCAGGGAATCTACTGACAGCTGACAATGGCCTTGGCGCCCAAGCCAGTAAGGCTG
      S L S V T V P V S H P V L N L S S P E D L I F E G A
1201  TGAGCCTCTCAGTCACTGTTCCCGTGTCTCATCTCTCACTCAGCTCTCTGAGGACCTGATTTTGTAGGGAGGCC
      K V T L H C E A Q R G S L P I L Y Q F H H E D A A L E
1281  AAGGTGACACTTCACTGTGAAGCCACAGAGAGGTTCACCTCCCATCTCTGTACCAAGTTTCATCATGAGGATGCTGCCCTGGA
      R R S A N S A G G V A I S F S L T A E H S G N Y Y C T
449
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FIGURE 6c-1A

1361	GGTAGTGGCCAACTCTGCAGGAGGAGTGGCCATCAGCTTCTCTGACTGCAGAGCAATTCAGGGAACTACTGTGCA	475
1441	A D N G F G P Q R S K A V S L S I T V P V S H P V L	
1521	CAGCTGACAATGGCTTTGGCCCCCAGCGCAGTAAGCGGTGAGCCTCTCCATCACTGTCCCTGTGTCTCATCTGTCCCTC	502
	T L S S A E A L T F E G A T V T L H C E V Q R G S P Q	
1601	ACCCTCAGCTCTGCTGAGGCCCTGACTTTTGAAGGAGCCACTGTGACACTTCACTGTGAAGTCCAGAGAGGTTCCCCACA	529
	I L Y Q F Y H E D M P L W S S S T P S V G R V S F S F	
1681	AATCCTATACCAGTTTATCATGAGGACATGCCCTCTGTGAGCAGCTCAACACCCCTCTGTGGGAAGAGTGTCTTCAGCT	555
	S L T E G H S G N Y Y C T A D N G F G P Q R S E V V	
1761	TCTCTGACTGAAGGACATTCAGGGAATTACTACTGCACAGCTGACAAATGGCTTTGGTCCCGCAGCGCAGTGAAGTGGTG	582
	S L F V T V P V S R P I L T L R V P R A Q A V V G D L	
1841	AGCCTTTTGTCACTGTTCCAGTGTCTCGCCCCATCCTCACCCCTCAGGGTCCCGAGGCCAGGCTGTGGTGGGGACCT	609
	L E L H C E A P R G S P P I L Y W F Y H E D V T L G S	
1921	GCTGGAGCTTCACTGTGAGGCCCGAGAGGCTCTCCCCCAATCCTGTACTGGTTTATCATGAGGATGTACCCCTGGGGA	635
	S S A P S G G E A S F N L S L T A E H S G N Y S C E	
2001	GCAGCTCAGCCCCCTCTGGAGGAGAAGCTTCTTTCAACCTCTCTCTGACTGCAGAACTTCTGGAACCTACTCATGTGAG	662
	A N N G L V A Q H S D T I S L S V I V P Y S R P I L T	
2081	GCCAAACAATGGCCTAGTGGCCCCAGCACAGTGACACAAATATCACTCAGTGTATAGTTCAGTATCTCGTCCCATCTCAC	689
	F R A P R A Q A V V G D L L E L H C E A L R G S S P I	
2161	CTTCAGGGCTCCAGGCCAGGCTGTGGTGGGGACCTGTGGAGCTTCACTGTGAGGCCCTGAGAGGCTCCTCCCCAA	715
	L Y W F Y H E D V T L G K I S A P S G G G A S F N L	
2241	TCCTGTACTGGTTTATCATGAAGATGTACCCCTGGTAAAGATCTCAGCCCTCTGGAGGAGGGCTCCTTCAACCTC	742
	S L T T E H S G I Y S C E A D N G L E A Q R S E M V T	
2321	TCTCTGACTACAGAACATTTCTGGAATCTACTCTCTGTGAGGCAGACAATGGTCTGGAGGCCCGCAGCGCAGTGGTGAC	769
	L K V A V P V S R P V L T L R A P G T H A A V G D L L	
2401	ACTGAAAGTTGCAGTTCGGTGTCTCGCCCGGTCTCACCCCTCAGGGCTCCCGGACCCATGTGCGTGGGGACCTGC	795
	E L H C E A L R G S P L I L Y R F F H E D V T L G N	
2481	TGGAGCTTCACTGTGAGGCCCTGAGAGGCTCTCCCCCTGATCCTGTACCGGTTTTCATGAGGATGTACCCCTAGGAAT	822
	R S S P S G G A S L N L S L T A E H S G N Y S C E A D	
2561	AGTTCGTCCTCCCTCTGGAGGAGCGTCTTAAACCTCTCTGACTGCAGAGCACCTCTGGAACCTACTCCTGTGAGGCCGA	849
	N G L G A Q R S E T V T L Y I T G L T A N R S G P F A	
2641	CAATGGCCTCGGGGCCCGCAGTGAGACAGTGTATATCATCAGGGCTGACCCCGAACAGAGTGGCCCTTTTG	875
	T G V A G G L L S I A G L A A G A L I L Y C W I S R	
	CCACAGGAGTGGCGGGGCTCTCTCAGCATAGCAGGCCCTGTCTGGGGGCGCACTGTCTACTGTCTGTCTCTCGAGA	902
	K A G R K P A S D P A R S P S D S Q E P T Y H N Y	

FIGURE 6c-1B

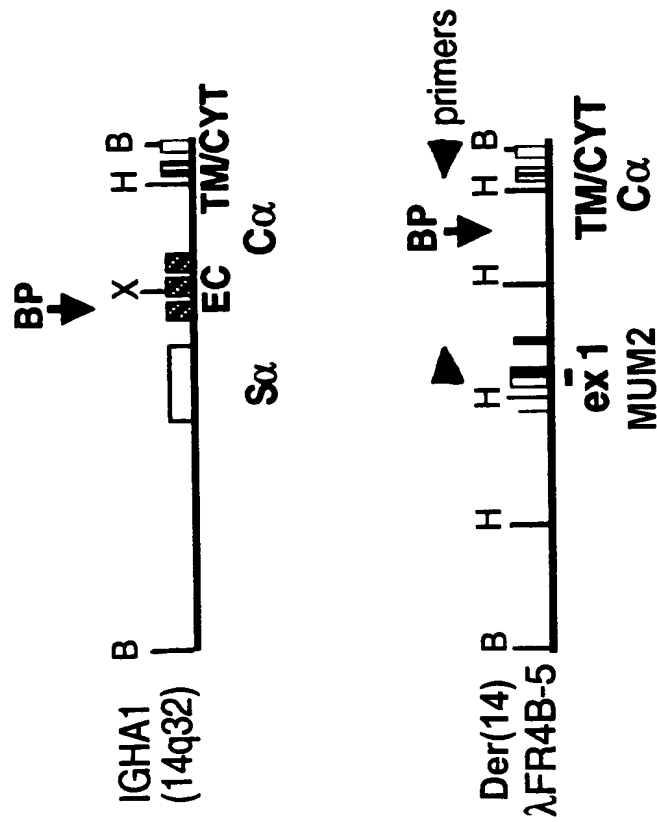
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    P A W E E L Q P V Y T N A N P R G E N V V Y S E Y R I 929
2801 ACCAGCCTGGGAAGAGCTGCCAACCCAGTGTAACACTAATGCCAAATCCTAGAGGAGAGAAATGTGGTTTACTCAGAAAGTACGGA
    I Q E K K K H A V A S D P R H L R N K G S P I I X S 955
2881 TCATCCAAGAGAGAAAGAAACATGCAGTGGCCTCTGACCCCGAGGCATCTCAGGAACAAGGGTTCCCTTATCATCTACTCT
```

FIGURE 6c-2

2961 E V K V A S T P V S G S L F L A S S A P H R * stop
3041 GAAGTTAAGGTGGCGTCAACCCCGTTTCCGGATCCCTGTTCTTGGCTTCTCAGCTCCTCAGATGAGTCCACACGTC
3121 TCTCCAACTGCTGTTTTCAGCTCTGACCCCAAGTTCCCTTGGGGAGAGCAGCATTTGAAGTGGAGATTTAGGCT
3201 GCCCCAGACCATATCTACTGGCTTGTTCACATGTCTCTCATTTCTCAGTCTGACCCAGAAATGACGGGCCCTGCTGGACTG
3281 TCACCTGTTTCCAGTTAAAGCCCTGACTGGCAGGTTTATTCAGTGGCAAGGTGCTCCACTCCAGGGCCACAGCAC
3361 ATCTCTGGATTCTTAGTGGGCTTTCAGCTGTGGTGTCTGTTCTGAGTACTGCTCTCATCACACCCACAGAGGGGGTC
3441 TTACCACACAAGGGAGAGTGGGCTTTCAGGAGATGCCGGGCTGGCTTAACAGCTCAGGTGCTCTTAACCTCCGACACAG
3521 AGTTCTGCTTGGGTGGATGCAATTTCTCAATTGTCTATCAGCTGTGGGCTACTGCGAGTGTGCTGCCAATATGGGACAG
3601 CACACAGCTGTGCACATGGACATGTGATGGGTCTCCACGGGGCTGCAATTTCACTCTCCACCTGCTCTCAAACT
3681 CTAAGGTCCGCACTTGACACCAAGGTAACTTCTCTCTGCTCATGTGTCAAGTGTCTACCTGCCCAAGTAAGTGGCTTTCA
3761 TACACCAAGTCCGAAGTTCTTCCCATCTTAACAGAAAGTAACCCAGCAAGTCAAGGCCAGGAGGACCCAGGGGTGCAGACA
3841 GAACACATACTGGAACACAGGAGGTCTCAATTAATTTGACTGACTGACTGAATGAATGAATGAATGAATGAATGAATGA
3921 TGTGGTAATCAAACTGGCATAAATCCAGTGCACCTCCCTAGGAAATCCGGGAGGTATTTCTGGCTTCTTAAGAAACAAG
4001 GAAGAGAAGGAGCTTGGATGAAGAACTGTTTTCAGCAAGAAAGGGCTTCTTTCACACTTTTATGTGCTTGTGATCACCT
4081 GAGGATCTGTGAAATAACAGATACTGATTGAGTGGGTCTGTGTAGAGCTGAGACTGCAATTTCTAATATGTTCCAGGGG
4161 ATGCTGATGCTGCTGGCCCTGGACTGCACTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT
4241 ATGCTGGCTCTGGCTGCCAGGGCCCACTCGGTTTACACGGATCTGTGCTGCTCCCTGGCCAGCTTTTGGCCACAGCAC
4321 CACCAGCTGCTGTGTGAGAGAGCTTCTTCTGTGACATGTTGGCTTTTCAATCAGCCACCTGGGAAGCGGAAGTAGC
4401 TGCCACTATCTTTGTTTCCCACTCAGGCTCAGCTTTCCTTCCATGAAAGGGTGAATGTATATTAACCTGAGCCCTCTCTCC
4481 ATTCAGAGTTGTTCTCCATCTCTGAGCAATGGGATGTTCTGTTCCGCTTTTATGATATCCATCATCTTATCTTGATC
4561 TTTGCTCCAGTGGATTGTACAGTGTGACTTTTAAAGCCCAAGGCTGAAATAAATCTTCCAGGGCAATTGGAAAGC
4641 TCACCTCCAGTGGATTGTACAGTGTGACTTTTAAAGCCCAAGGCTGAAATAAATCTTCCAGGGCAATTGGAAAGC
4721 CAACCTTTCAGAGGAGGAACCCAGACACCTGAGACAGGAGCTGTATGACGCCCTGAGTGCAGCTTGCAGAGGACAAAGGCTG
4801 GAGGCAATTTGTCATCACTACAGATATGCAACTAAATAGACGTGGAGCAAGAGAAATGCAATTTCCACCGAGCCGCTTTT
4881 TTAGGCTAGTTGAAAGTCAAGAGGACAGCAGCAAGCATAGGCTCAGGATTAAGAAATAAATCTGCTCACAGTCTGTT
4961 CTGGAGGTCACATCACCACAAAGCTCAGCCCTATGCAAGTTCTGAGAAAGTGGAGGCAAGGCTCAAAAGAGGAAATTT
5041 TAGAATTTCTCATTTGGGAGAGTAAGGTACCCCTTCCAGAAATGATTAATGTCACAGTGGCAGAACTCCACCCCTAAT
5121 GTGGGTGGACCCCATCCAGTCTGTTGAAGGCTGAAATGTAACAAAGGGCTTATTTCTTCTCAAGTAAGGGGAACTCCT
5201 GCTTTGGGCTGGACATAAGTTTTTCTGTTTTCAGACGCAAACTGAAATGGCTCTTCTTGGGTCTTGAGCTTGTGGC
5281 ATATGGACTGAAGAAACTATGCTATTGGATCTCTGGATCTCCAGCTTGCTGACTGAGATCTTGAGATATGTCAGCCT
CTACAGTCAAGAGCTAATTCATTTCTAATAACCAATCTTTTC

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FIG. 7A



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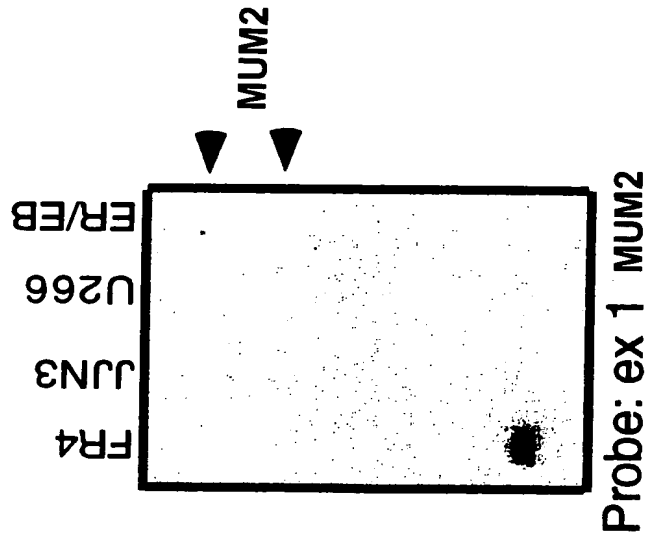


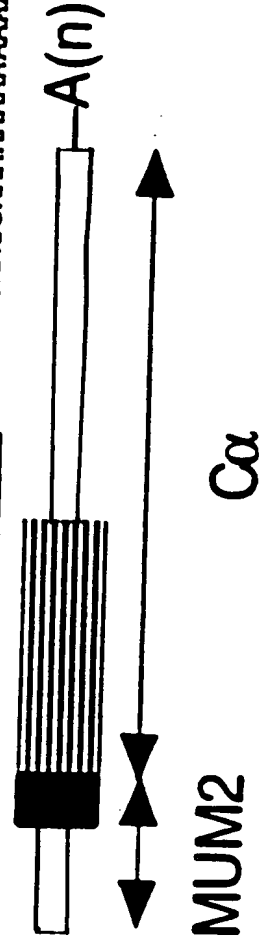
FIG. 7B

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FIG. 7C

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1  CTCAATCAGCTTTATGTCAGAGAGAAGCTTACTGAGCTCACTGCTGGTGGTGTAGGCAAGTGC'TGCTTTGGCAA
78  TCTGGGCTGACCTGGCTTGTCTCAGAACTCCTTCTCAACCCCTGGAGCAGGCTTCCATGCTGCTGGGCGTCC
   L L A F A P V C G Q S G S C S V A D W Q M P P P Y V
155 TTGCTGGCCTTTGCTCCAGTCTGTGGACAATCTGGCTCTTGTCTGTTCAGATTGGCAGATGCCCGCTCCCTATGT
   V L D L P Q E T L E E T P G A N L W P T T L T F L
232 GGTGCTGGACTTGGCCGAGGAGACCCCTGGAGGAGACCCCGCGCCCAACCTGTGGCCCCACCACCATCACCTTCC
   T L F L L S L F Y S T A L T V T S V R G P S G N R
309 TCACCCCTCTTCCTGCTGAGCCTGTTCTATAGCACAGCACTGACCCGTGACCCAGCGTCCGGGGGCCCATCTGGCAACAGG
   E G P Q Y .
386 GAGGGCCCCCAGTACTGAGCGGGAGCCGGCAAGGCACAGGTGGGAGCCCCAGGAGGGGATGAGCCACAGTGGATGA
463 GGTGGGCTGCAGTGTGGCTAAGAGGAGAGCACCACTGCTCCCACTGTGGGGGACGTGCTCTCTGGGGGGCCCC
540 TTCACAGACACTGAGGACACGCGAGGCCCCAGGTCAGGGCTGAGCTTCCCTCCAGTGCAGTAACGAGGATTCCGTC
617 CAGGCTCCCATGAGCAGGCCAGGGCTGAGACAGAGGGCGTTGGCAAGGATGCTGCTCTTCAGGCTGTGACCCCTCTG
694 TCTTTGCAGGGAGGAAGTGTGGAGGAACCTCTTGGAGAAGCCAGCTATGCTTGGCCAGAACTCAGCCCTTTCAGACGT
771 CACCGACCCGCCCTTACTCACAATGCTCCAGGTGCAATAAGTGGCCCCCAAGGAAAAA
  
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FIGURE 8A

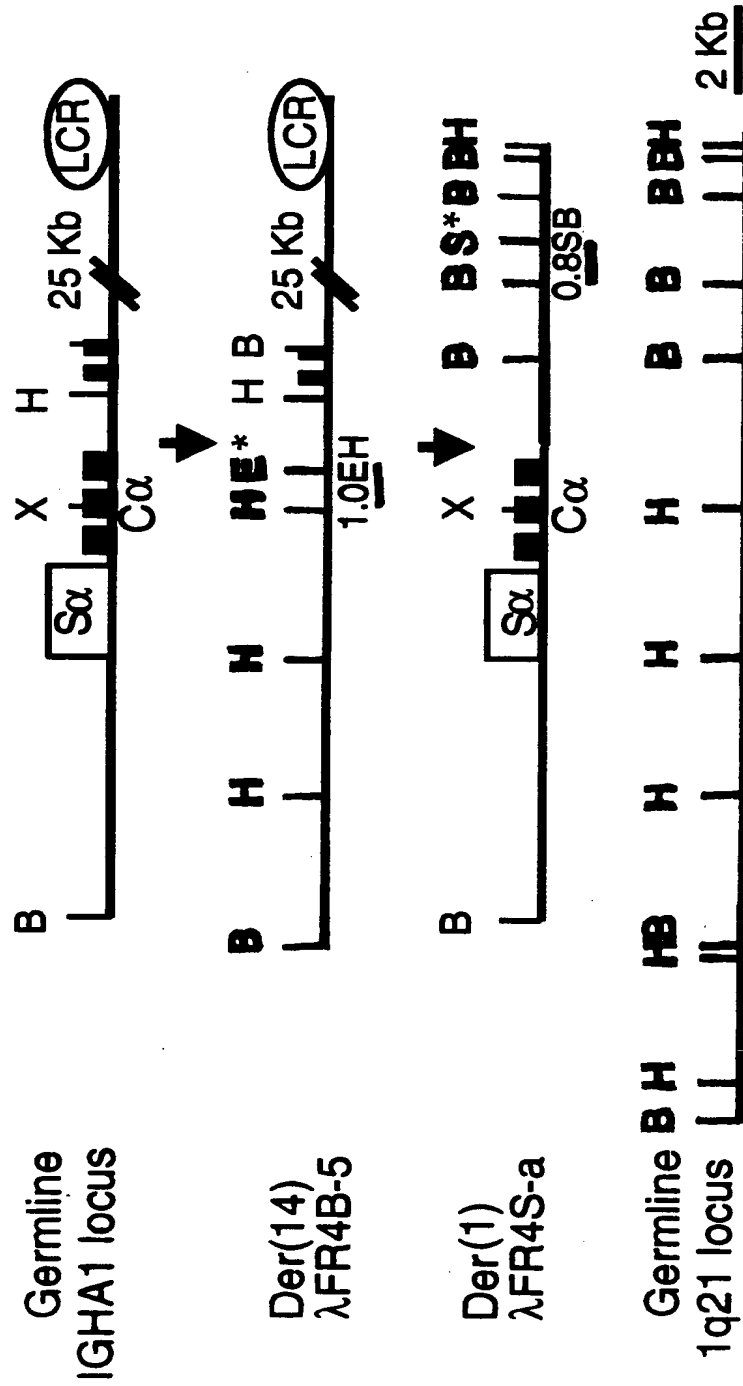
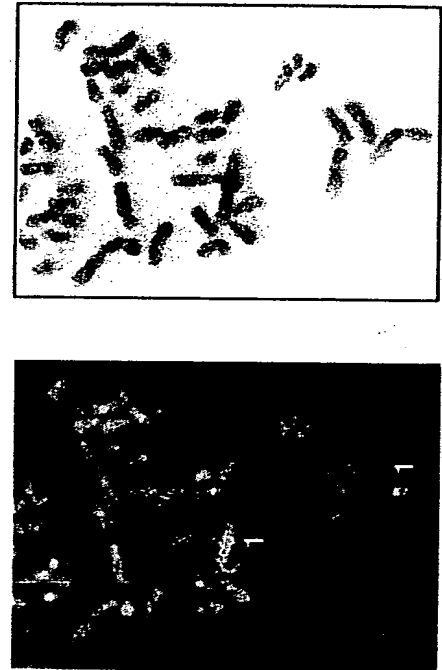


FIG. 8B

Chr 14 TCCCACTGACGCATGCAGGAAGGGCACCTCCCTTAACCACTGCTCTGTACGGGGGACGTTGGGCACAGTGCACACTCACA
 Der (14) GGCCTGACAGCAACTTTTCTTCTACTAGTTCATCTTAA-CAACTGCTCTGTACGGGGGACGTTGGGCACAGTGCACACTCACA
 Chr 1 GGCCTGACAGCAACTTTTCTTCTACTAGTTCATCTTAACTTATCCTGTAACCTGGGAGACAACTGTCTTAAGTAACTGAAGGGAAA
 Chr 1 GGCCTGACAGCAACTTTTCTTCTACTAGTTCATCTTAACTTATCCTGTAACCTGGGAGACAACTGTCTTAAGTAACTGAAGGGAAA
 Der (1) TCCCACTGACGCA-----GGAAGGATCTTAAAGTTTATCCTGTAACCTGGGAGACAACTGTCTTAAGTAACTGAAGGGAAA
 Chr 14 TCCCACTGACGCA TGCAGGAAGGGGACCTCCCTTAACCACTGCTCTGTACGGGGGACGTTGGGCACAGTGCACACTCACA

FIG. 8C



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FIG. 9A

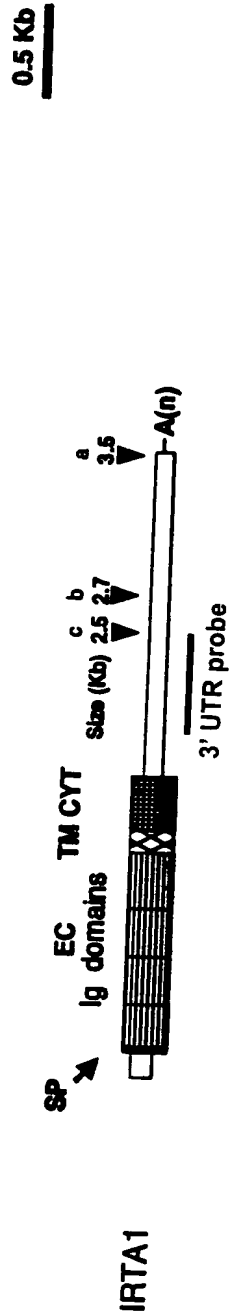
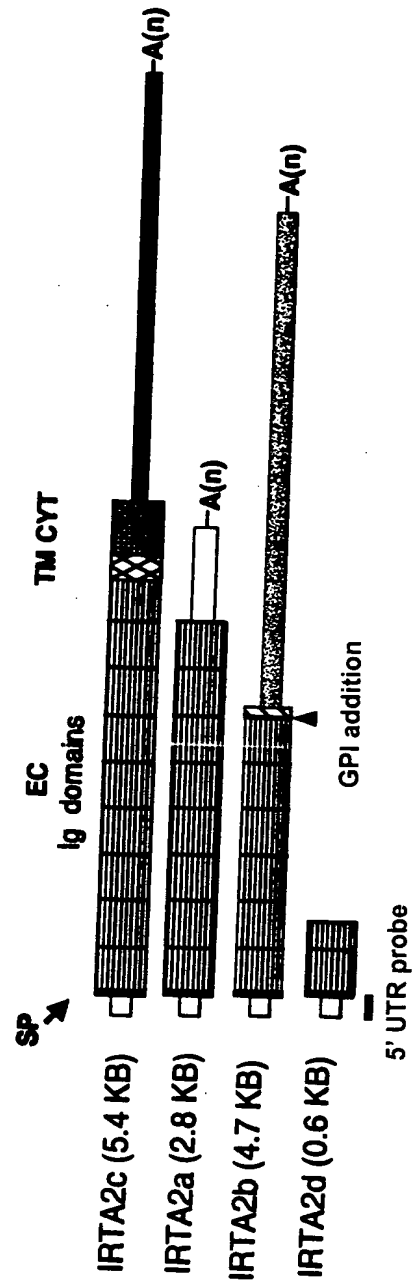


FIG. 9B



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FIGURE 10A

FCGR1IA	(1)	MAMETQMSQNVCPRNLLWLLQPPVLLVLLASADSSAAAPKAVLKLEPPMIMVLQEDSVLTLCQCCARSPESDSIQWPHNGNIIPTHIQPSYRFRKNNNDSC
FCGR1IIA	(1)	-----MWQLPPPAHLLVSAGMRTEDLPAAVVFLPQAYRMLEKDSVTLKQCCAYSPEDNSTQWPHNESIISQAASSYFIADAVYDSC
FCERIA	(1)	-----MAP-AMESPPTLCVADIEFAPDCVLAVPQPKVSLNPPNRIEKGENVLTQGNNEFEVSSSTQWPHNGSISETNSSLNIVNKKFPDSC
FCGR1A	(1)	-----MWFLTTLVLLWVPVGDGV-DTIAVATISLQPPVSVFQBEAVTLHCDEVLHIFGSSSTQWPHNGSISETNSSLNIVNKKFPDSC
IRTA-1	(1)	-----MLTWASLTLAFAPVCEQSAAHKPVLSVHPPTTFEKGENVLTQGNCFQFYATEKTIYERHYWGEKLLITPGNT-LEVRPESC
IRTA-2	(1)	-----MLTWVTLVLPVSGCFARTERPILFLOPPMTVFEQGERVTLTKCFRFPYSPQKTKYERHYLKGKILRETTPDNI-LEVQESC
FCGR1IA	(101)	EVTCCQTGQTSLSDPVHETVLSWLVLTQTEHLEFCQGETIMLRCHSMKDKPPLVAVTFFQNGKSKQESRLDPTESIPQANHSHSDPHCTGNIQVTL-FSSK
FCGR1IIA	(86)	EVRCQTNLSLTSDPVQTEVHIGWLLQAFRWVEKEDEIHLRCHSMKNTAPLHNAVTLQNGSGRKYFHHNSDEYIEKETLKESSMFCRGLFESKN-VSSK
FCERIA	(90)	EVKCCHQVNESEPVYLEVFSDWLLLOQASAEVVMGCEPLFRCHGGRNWDVAKVIVYKDCGALIVYWEHNISITNAVVELSETVYCTGCKVWQLD-YESE
FCGR1A	(82)	EVRCQGLSGRSDFIQLEIHRGWLLQVSSRVFTEGEPALARCHAMRDKLVINVLVYRNGKAFKFFHWSNLTLTKTNI SHNGTYHSG-NCKHR-YTSA
IRTA-1	(82)	LYRCQARGSPRNPVRILFSSDSLLOAFYSVFEGDTLVLRCHRRRKEKLTAKKVTWNGNIISISNKSMDLLIFQASSNNNGNRGITYGDENDVFRSN
IRTA-2	(82)	BYRCQAQGSPTSSPVHIDFSSASLLOAELSMFEGLSVLRCHRAKAEVTLANNITIK-NDNVPLAENKRITDEHIFPAACLKQNCARCGCYKESCCPVSSN
FCGR1	(172)	CKHR--YTSAGISVTVKELFFAPVLNASVTSLELLEGNLVTLSCETKILLQRPGLQLVESEFYMGSLTL-RGRNTSSEYQILLTARRPDSGLTWCEAAIEDGN
IRTA-1	(171)	EDENDVFRSNFKITKIQDELFFHFEIKATDSQI-TEGNSVNLSCETQPPERSDTPLHNEFRDGEVILSDWSTYPEILQLPVWRENSGSLTWCGFETVRGN
IRTA-2	(170)	KECCCPVSSNTVYKIQVQEFETRPVTRASSFOI-ISENPVLTICETQUSLERSDVLRREREEDQILGLGMSLSSENFOTITAMSKDSGFYWCNATMPHS
FCGR1	(269)	VLRSPFELQVLGLQLPTPVWFHVLGYLAVGIMFLVNVLVWVIRKEEXRKKKKWDLEISLDSGHEKVTSSLOEDRHLLEELKQCE-OKEEQIQEQGVHR
IRTA-1	(270)	IHKHSPSTQTHVGRIPVSGVL-LETQISGGQAVEGEMLVVCVAEGTGDITFSWHRDMDQESLGNKTQRSRAELETPAIRQSHAG-CMYCTADNSYC-
IRTA-2	(269)	VISDSPRSWIOVG-IRASHPV-LTISPEKALNFECTKVTLHCETOEDSIRTDYRFYHEGV--PIRHKSVRCERGASISFSLTTENSE-NVYCTADNGLCA

FIGURE 10B

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E      E      I      I
DTM:  DXXXXXXX--DXX--YXXLXXXXXXXX--YXXL

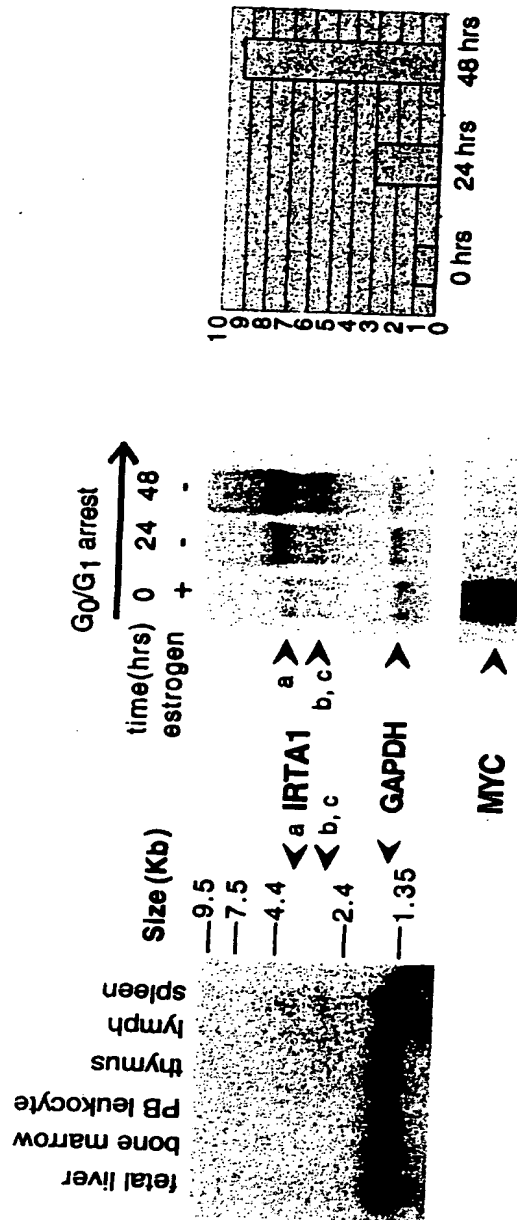
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IRTA-2C:  DSDSQ---EPTYHNVPAAEELQPVYT-----NANPRGENVVYSEV
BGP-1:    ASDQR---DLTEHKPSVSNHQTQDHSN-----DPPNKMNEVTYSTL

ITIM:     SXYXXL      SXYXXL      SXYXXL
          V      V      V      V      V      V
          L      L      L      L      L      L
          I      I      I      I      I      I

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FIGURE 11A

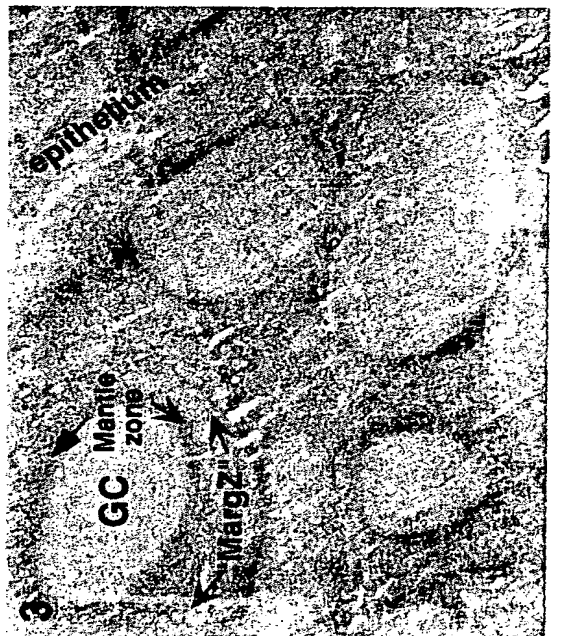
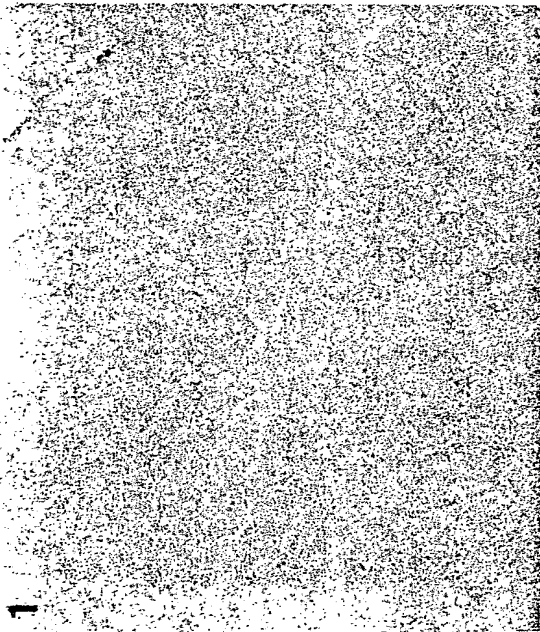


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FIGURE 11B1-B4

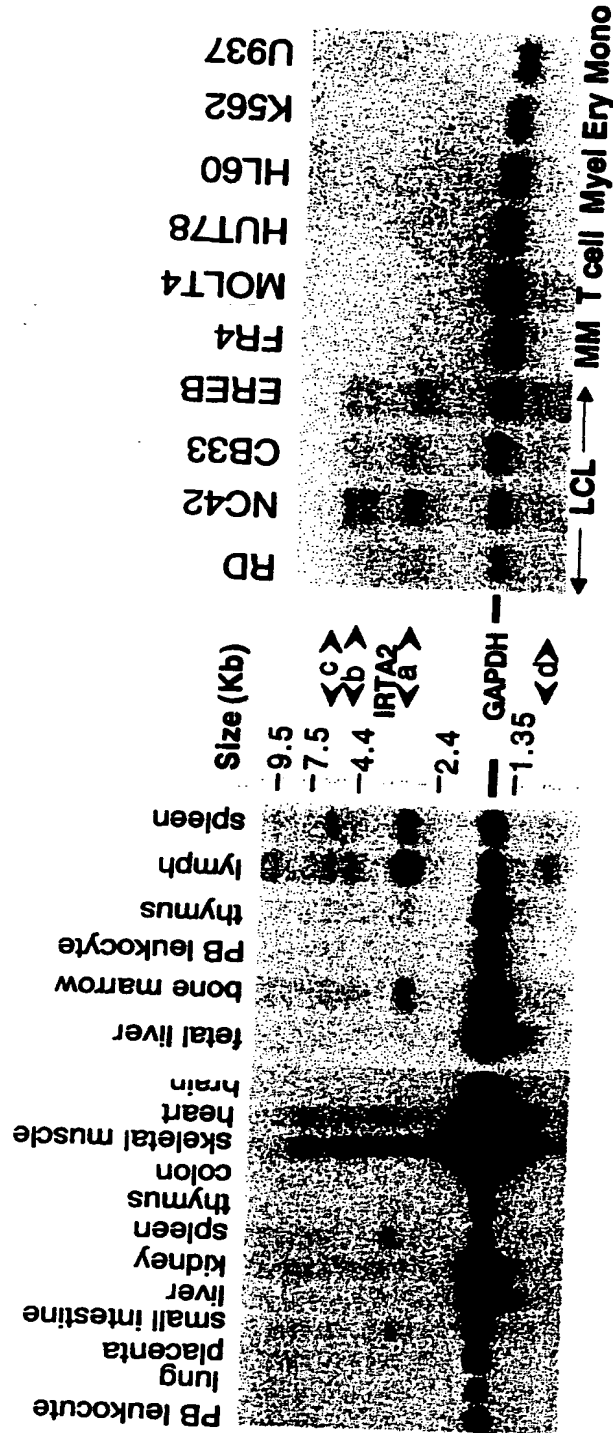
11B1-4



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FIGURE 12A

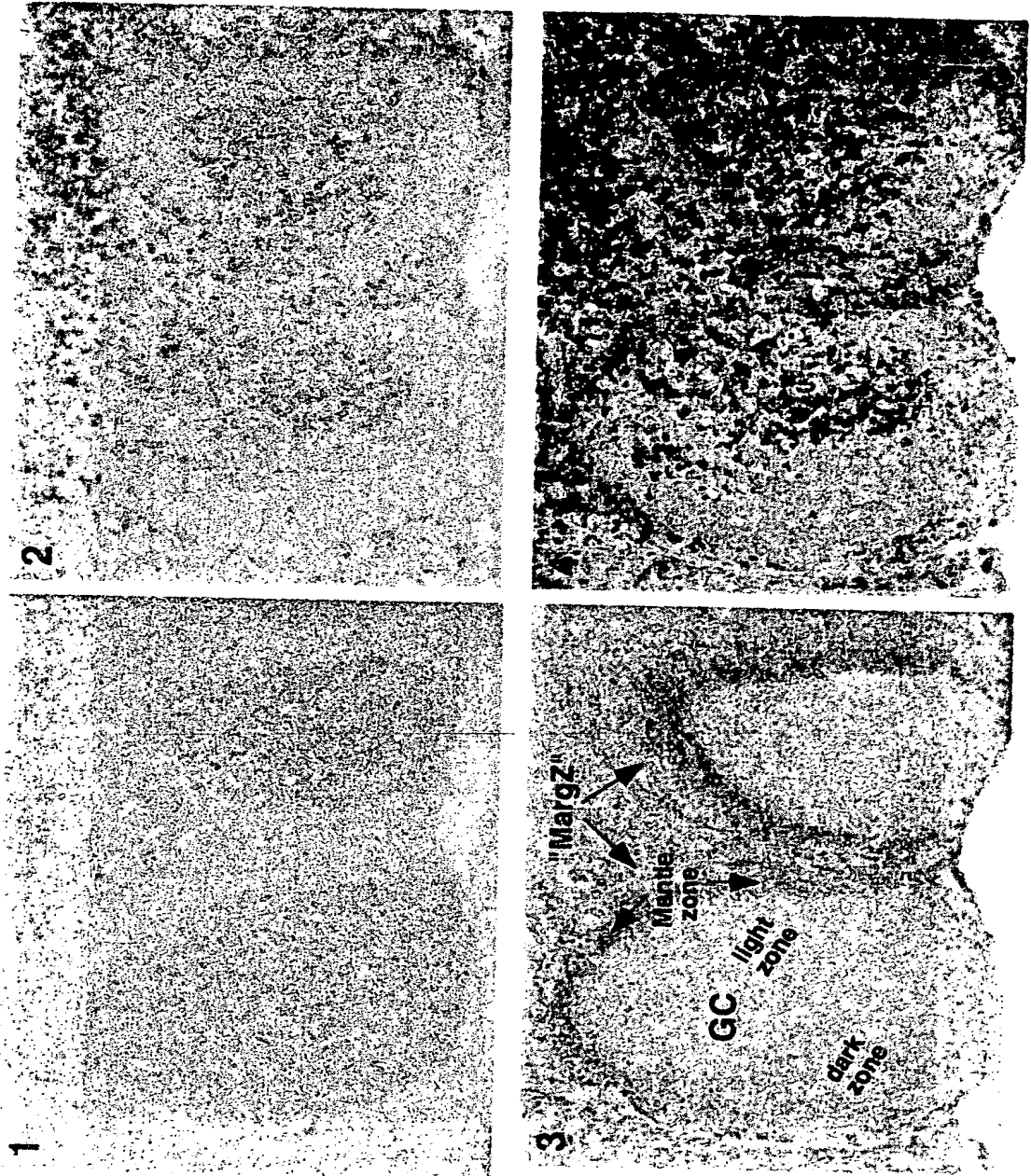


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FIGURE 12B1-B4

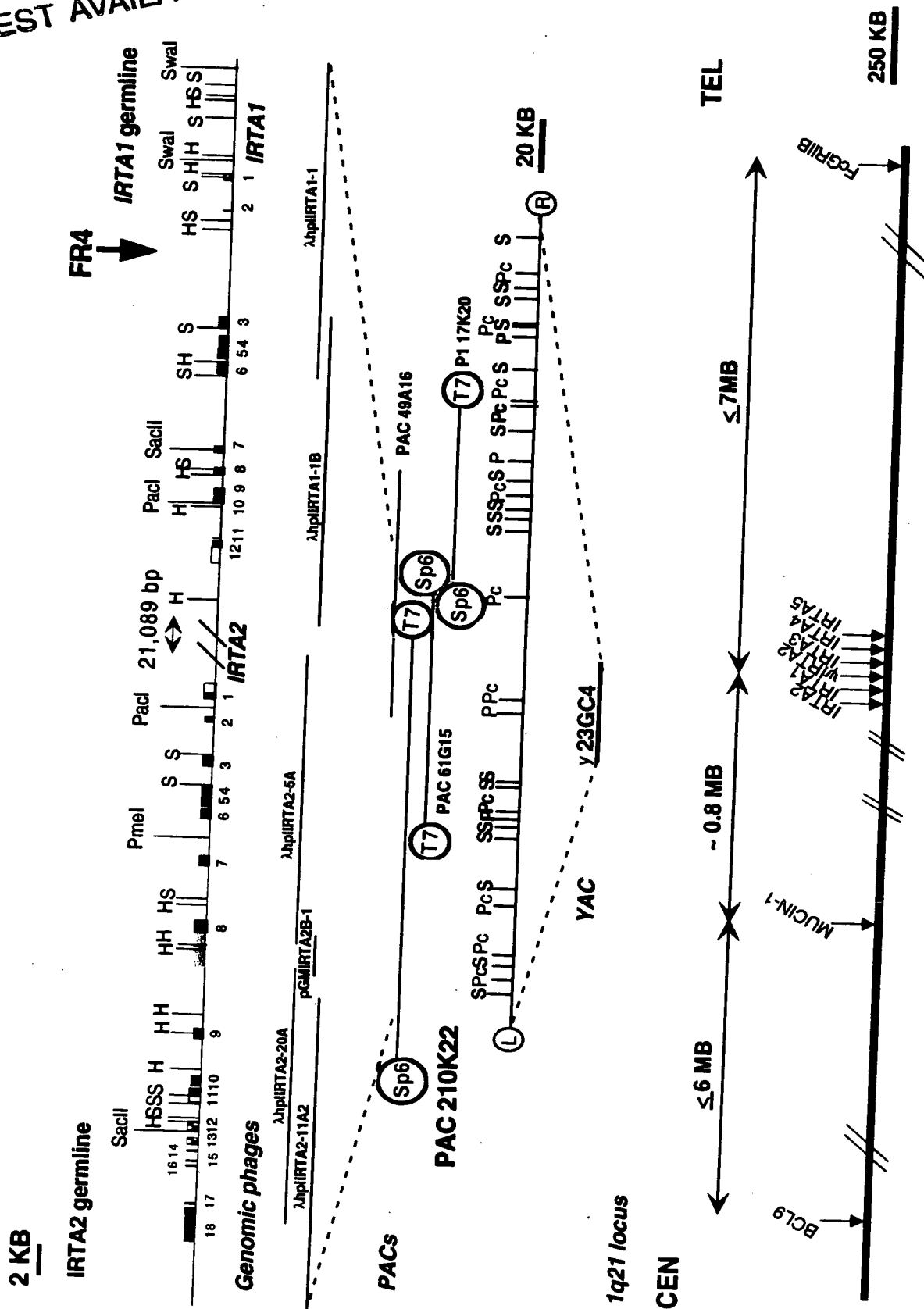
B



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FIGURE 13



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FIG. 14B

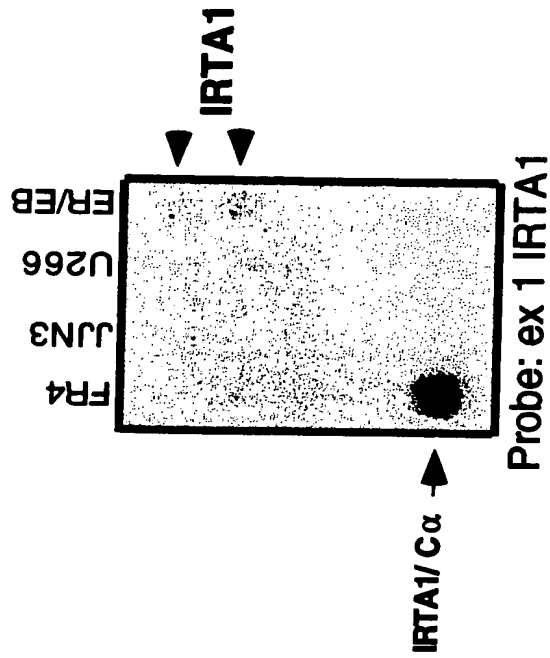
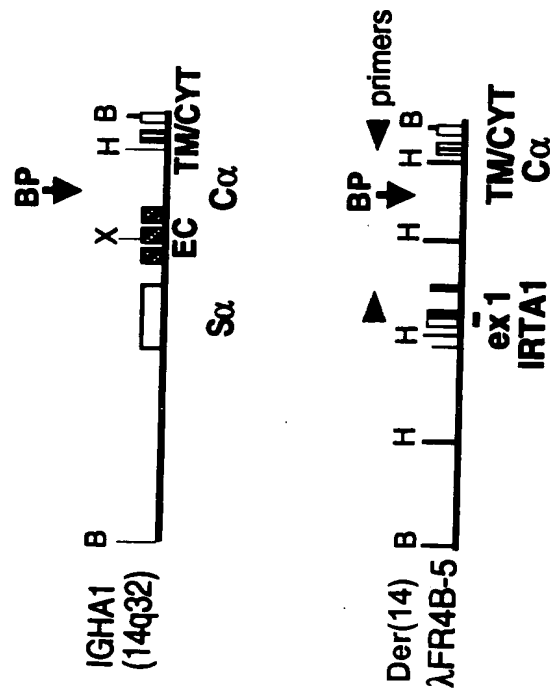


FIG. 14A



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FIG. 14D

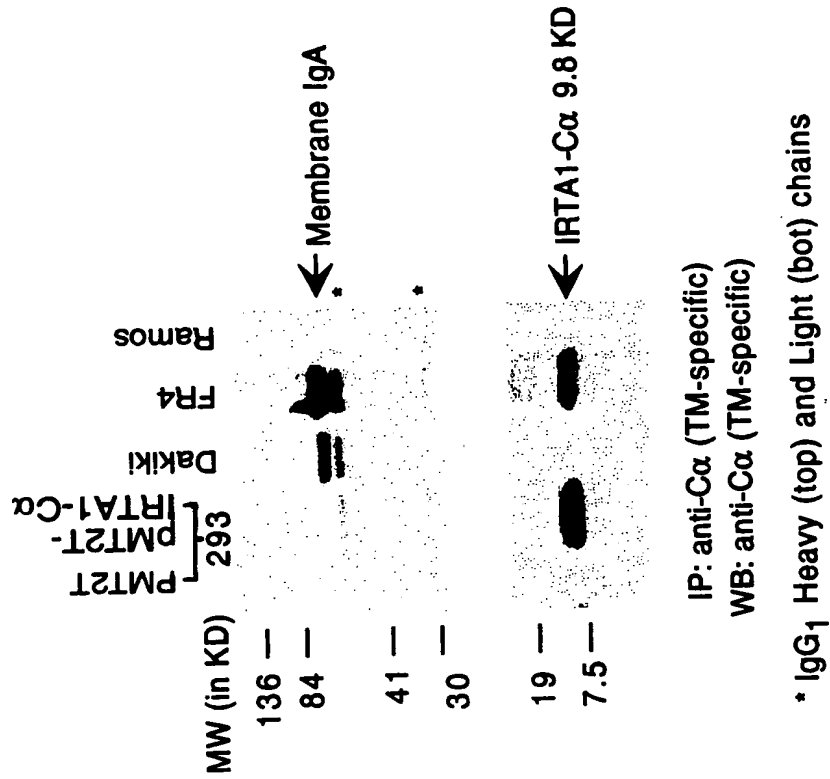
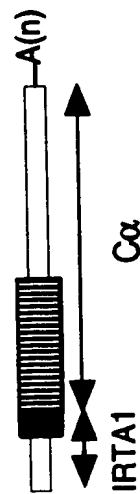
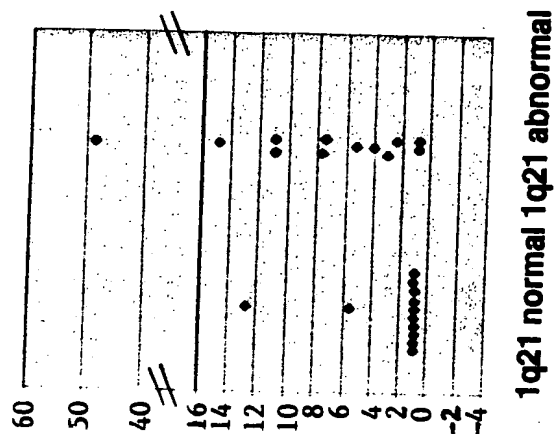


FIG. 14C



1q21 normal 1q21 abnormal



FR4 U266 JUNG EJM SKRM1 YG1 YG2 YG4 YG6 YG7

IRT A2 { c =
b =
a —

GAPDH →
IRT A2 d —

+ - - - - - + - - - - - +

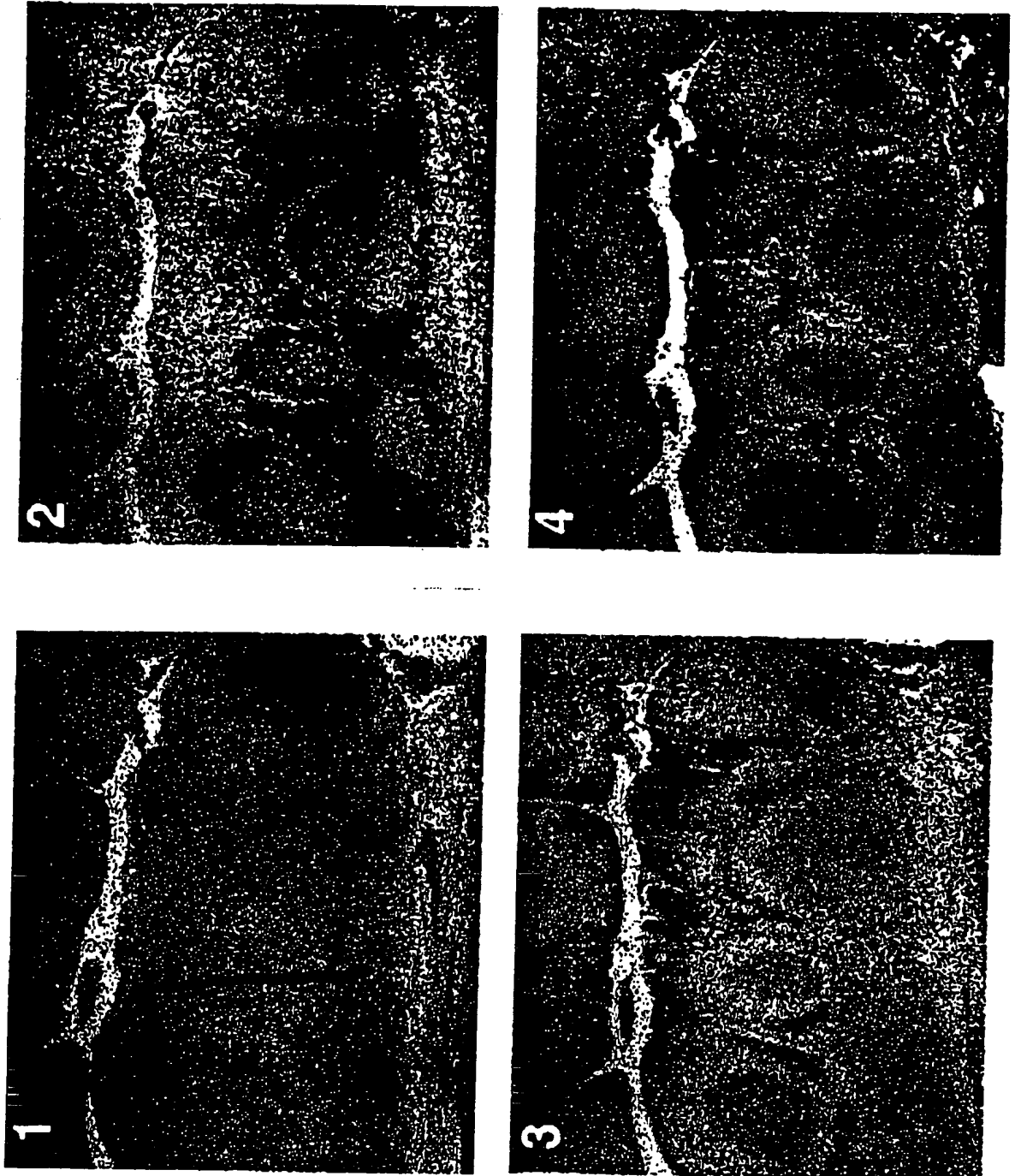
1q21 cytogenetic abnormality

| Cell line | IRTA2 |
|--------------------------------|--------------|
| <i>Burkitt Lymphoma</i> | |
| Normal 1q21 | 2/12 |
| Abnormal 1q21 | 10/12 |
| <i>Multiple Myeloma</i> | |
| Normal 1q21 | 0/7 |
| Abnormal 1q21 | 1/3 |

Summary of *IRTA2* expression

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FIGURE 16-1~16-4
IRTA1 expression in normal lymphoid tissue

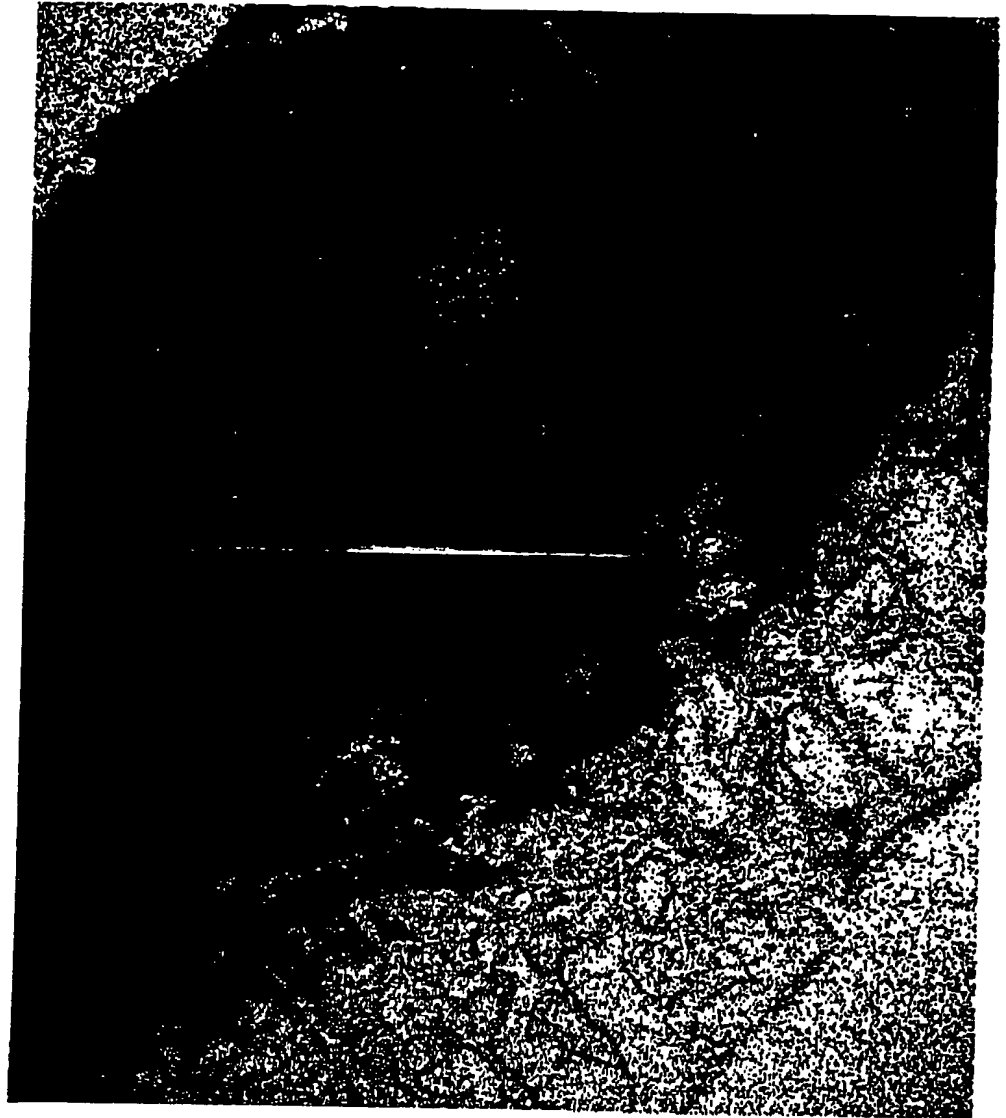


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FIGURE 17

IRTA1 expression in a stomach Mucosa-Associated-Lymphoid Tissue B cell lymphoma



1 CTCAATCAGCTTATGCAGAGAAGCTTACTGAGCTCACTGCTGGTGTGCTGGTGGCAAGTGTGCTTTGGCAA 6 M L L W A S

78 TCTGGGCTGACCTGGCTTGTCTCTCAAACTCCTTCTCCAAACCTGGAGCAGGCTTCCATGCTGTGTGGCGTCC L L A F A P V C G G S A A A H K P V I S V H P P W T 32

155 TTGCTGGCCTTGTCTCCAGTCTGTGGACAATCGAGCTGCACACAAACCTGTGATTCCTCGTCCATCCTCCATGGAC T F F K G E R V T L T C N G F Q F Y A T E K T T W Y 58

232 CACATTCTTCAAGGAGAGAGTGTGACTCTGACTTGCATGCAATGGAATTCAGTTCTATGCAACAGAGAAACAACATGGT H R H Y W G E K L T L T P G N T L E V R E S G L Y 83

309 ATCATCGGCACTACTGGGAGAAAAGTTGACCTGACCCAGGAACACCCCTGAGGTTTCGGGAATCTGGACTGTAC R C Q A R G S P P S N P V R L L F S D S I L Q A 109

386 AGATGCCAGGCCGGGCTCCCCACGAAGTAACCCCTGTGCGCTCTCTTTTTCITCAGACTCCTTAATCTGCAGGC P Y S V F E G D T L V L R C H R R R K E K L T A V K 135

463 ACCATATTCTGTGTTGAGGTCGACACATTTGTTCTGAGATGCCACAGAAGAGGAAGAAATGACTGCTGTGA Y T W N G N T L S I S N K S W D L I P Q A S S N 160

540 AATATACTTGGAAATGAAACATCTCTTCCATTTCAATAAAAGCTGGGATCTTCTATCCCAAGCAAGTTCAAAT N N G N Y R C I G Y G D E N D V F R S N F K I I K I 186

617 AACAAATGGCAATATCGATGCAATGGATATGGAGATGAGAATGATGATTTAGATCAAAATTTCAAATATATTAAT Q E L F P H P E L K A T D S Q P T E G N S V 212

694 TCAAGAACTATTTCACATCCAGAGCTGAAAGCTACAGACTCTCAGCCTACAGAGGGAATTCGTAAACCTGAGCT E T Q L P P E R S D T P L H F N F R D G E V I L 237

771 GTGAACACACAGCTTCTCCAGAGCGGTGAGACACCCCACTTCACTCAACTTCTTCCAGAGATGGCGAGTCACTCGT S D W S T Y P E L Q L P T V W R E N S G S Y W C G A 263

848 TCAGACTGGAGCAGTACCCGGAATCCAGCTCCCAACCGTCTGGAGAGAAAACCTCAGGATCCTATTGGTGTGGTGC E T V R G N I H K H S P S L Q I H V Q R I P V S G V 289

925 TGAACACAGTGAGGGTAACATCCACAAGCACAGTCCCTCGTACAGATCCATGTGACGGGATCCCTGTGTCTGGG L L E T Q P S G G Q A V E G E M L V L V C S V A E 314

1002 TGCTCCTGGAGACCCGCTCAGGGGGCCAGGCTGTGAAGGGAGATGCTGGTCTGTCTGTCTCCGTCCGTGGGTGAA G T G D T T F S W H R E D M Q E S L G R K T Q R S L 340

11079 GGCACAGGGGATACCAATTTCTCTGGCACCGGAGGACATGCAGAGAGTCTGGGAGGAAAACCTCAGCGTTCCCT R A E L E L P A I R Q S H A G G Y Y C T A D N S Y G 366

1156 GAGAGCAGCTGGAGCTCCCTGCCATCAGACAGAGCCATGCAGGGGATACTACTGTACAGCAGACAACAGCTACG P V Q S M V L V T V R E T P G N R D G L V A A G 391

1233 GCCCTGTCCAGAGCATGGTGTGAATGTCACTGTGAGAGAGACCCAGGCAACAGAGATGGCCTTGTGCGCGCGGA A T G G L L S A L L L A V A L L F H C W R R R K S G 417

1310 GCCACTGGAGGCTGCTCAGTGTCTTCTCCTGGCTGTGGCCCTGTGTTTCACTGCTGGCGTCGGAGGAAGTACGG V G F L G D E T R L P P A P G P G E S S H S I C P A 443

1387 AGTTGGTTTCTTGGGAGACGAACACAGGCTCCCTCCCGCTCCAGGCCAGGAGAGTCTCCCATTCCTATCTGCCCTG

FIGURE 18AA

1464 Q V E L Q S L Y V D V H P K K G D L V Y S E I Q T 468
CCCAGGTGGAGCTTCAGTCGTTGTATGTTGATGTACACCCCAAGGAGATTTGGTATACTCTGAGATCCAGACT
1541 T Q L G E E E A N T S R T L L E D K D V S V Y S 494
ACTCAGCTGGGAGAAGAGGAAGCTAATACCTCCAGACACTTCTAGAGGATAAGGATGTCCTCAGTTGCTACTC
E V K T Q H P D N S A G K I S S K D E S * 515
1618 TGAGGTAAAGACACAAACCCAGATAACTCAGCTGGAAGATCAGCTCTAAGGATGAAGAAAGTTAAGAGAATGAAA
1695 AGTTACGGGAACGTCTACTCATGTGATTTCTCCCTTGTCCAAAGTCCAGGCCAGTGCAGTCCCTTGCAGCACCTG
1772 GAATGATCAACTATCCAGCTTTCTAATTTCTCATGATATGCAATTCACCTCCAGGAATACATCTCGTCTACT
1849 CTGATGTTGGGATGGAATGGCCTCTGAAGACTTCACTAAATGACCAGGATCCACAGTTAAGAGAAGACCCCTGTAG
1926 TATTTGCTGTGGGCTGACCTAATGCATTTCCCTAGGCTCTGTTAGAGAAGGGGATAAAGAGAGAGAAGGACTGT
2003 TATGAAAAACAGAGCACAAATTTTGGTGAATTTGGGATTTGCAGAGATGAAAAGACTGGGTGACCTGGATCTCTGC
2080 TTAATACATCTACAAACCATTTGCTCACTGGAGACTCACTTGCATCAGTTTGTAACTGTGAGTGGCTGCACAGGCA
2157 CTGTGCAACAATGAAAAGCCCCCTTCACTTCTGCTGAGAGATTAAGAGAGGACATCAGAAGAGCTGGAGATGCAAGCTCTAGGCTGC
2234 CCCATCTGGAATGGTTTACAGAGAGAGGAATTTAAAGAGGAGGACATCAGAAGAGCTGGAGATGCAAGCTCTAGGCTGC
2311 GCTTCCAAAAGCAAAATGATAATTATGTTAATGTCATTAGTGACAAAAGATTTGCAACATTAGAGAAAAGAGACACAAA
2388 TATAAAATTAATAAACTTAAGTACCAACTCCAAAACCTAAATTTGAACCTTAAATATTAGTATAAACTCATAATAA
• CTCTGCCTTTTAAATAAAAAAAAAAAAAAAAAAAAAA

IRTA1 cDNA and protein sequence

[illegible]

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FIGURE 18B-1A

```
1361 GCGTAGGTCGGCCAACTCTGCAGGAGGTGGCCATCAGCTTCTCTCTGCTGACAGAGCAATTCAGGAACTACTACTGCA 475
      A D N G F G P Q R S K A V S L S I T V P V S H P V L
1441 CAGCTGACAAATGGCTTTGGCCCCCAGCGAGTAAGCGGTGAGCCCTCTCCATCACTGTCCCTGTGTCTCATCCTGTCTCTC
      T L S S A E A L T F E G A T V T L H C E V Q R G S P Q 502
1521 ACCCTCAGCTCTGCTGAGGCCCTGACTTTTGAAGGAGCCACTGTGACACTTCACTGTGAAGTCCAGAGAGGTTCCTCCAC
      I L Y Q F Y H E D M P L W S S T P S V G R V S F S F 529
1601 AATCCTATACCACTTTTATCATGAGGACATGCCCCCTGTGGAGCAGCTCAACACCCCTCTGTGGGAAGAGTGTCTCTTCAGCT
      S L T E G H S G N Y Y C T A D N G F G P Q R S E V V 555
1681 TCTCTCTGACTGAAGGACATTCAGGGAATTACTACTGCACAGCTGACAATGGCTTTGGTCCCCCAGCGCAGTGAAGTGGTG

      S L F V T V P V S R P I L T L R V P R A Q A V V G D L 582
2A,2C1761 AGCCTTTTGTCACTGTCCAGTGTCTCGCCCCCATCTCACCCCTCAGGGTTCCAGGGCCCCAGGCTGTGGTGGGGACCT
      G K C W V L A S H P P L A E F S L T H S F K 582
2B 1761 -----GGTAAGTGTGGGTCTTGCCAGTCACCCACCCCTGGCTGAGTTCTCTCTCACCCCATTCCTTTAA

      L E L H C E A P R G S P P I L Y W F Y H E D V T L G S 609
2A,2C1841 GCTGGAGCTTCACTGTGAGGCCCCGAGAGGCTCTCCCCCAATCCTGTACTGGTTTATCATGAGGATGTCACCCCTGGGGA
      N L F A L S S F L P * stop 592
2B 1841 AAATCTGTTTGCACTGTCAGTTTCTCCCTTAATCAACTTAATCCCTTCTTGGCTTCTCTCACTCAACTAAGTGGG

      S S A P S G G E A S F N L S L T A E H S G N Y S C E 635
2A,2C1921 GCAGCTCAGCCCCCTCTGGAGGAGAAGCTTCTTCAACCTCTCTGACTGCAGAACATTCCTGGAATCTACTCATGTGAG
      GTTTCCGTAATCAAGTCTGGCTCAGCCAGACCCCTAAACAGCTCAGTAGATTCCTCCAGCTTTTACCAAATGAATT
      A N N G L V A Q H S D T I S L S V I V P V S R P I L T 662
2A,2C2001 GCCAACAAATGGCCTAGTGGCCCCAGCACAGTACACAATATCACTCAGTGTATAGTTCAGTATCTCGTCCCATCCTCAC
      TATTTATTGTATTTTCTCTCATTCCTTTGTATGTTCCACACAGTACGCCCAATTTTCTTGTATGCACGGGCGTGTCTCTACT
      F R A P R A Q A V V G D L L E L H C E A L R G S S P I 689
2A,2C2081 CTTCAGGGCTCCCAGGCCCCAGGCTGTGTGGGGACCTGTGGAGCTTCACTGTGAGGCCCTGAGAGGCTCCTCCCCCAA
      TCTCTACTGACATTTACATATTAACCTTAGCTACAAGCACAGCTTATAGATAAATATGGTCAAGACCTTAAATTTCTCCA
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| | | |
|------------|---|-----|
| 2A, 202161 | L Y W F Y H E D V T L G K I S A P S G G A S F N L | 715 |
| 2B 2161 | TCTGTACTGGTTTATCATGAAGATGTACCCCTGGGTAGATCTCAGCCCCCTCTGGAGGAGGGCCCTCCTTCAGCTC | |
| 2B 2161 | AAGGATTTCCAACTTATGGTAGATTGGAGAAAGCTGCTGGTGAACAAGGGGAAATGGCTCCCTAGGAACCAACTCC | |
| 2A, 202241 | L T T E H S G I Y S C E A D N G L E A Q R S E M V T | 742 |
| 2B 2241 | TCTCTGACTACAGAACATCTGGAAATCTACTCTGTGAGGCAGACAAATGGTCTGGAGGCCAGCGCAGTGAGATGGTGAC | |
| 2B 2241 | TCAAACCTCTGGAGTTTTATGATCCCTTGTCTTCTAACCTGTCTAAATCAGTATCATTTTATGTATTATTTTAAAAAA | |
| 2C 2321 | L K V A V P V S R P V L T L R A P G T H A A V G D L L | 769 |
| 2B 2321 | ACTGAAAGTTGCGATTCGGCTGCTCGCCCGGTCTCACCCTCAGGGCTCCGGGACCCATGCTGCGGTGGGGACCTGC | |
| 2A 2321 | -----G E W A L P T S S T S E N * | 759 |
| 2B 2321 | -----GGTGAGTGGGCCCTGCCCCACCAGCAGCACATCTCAGAACTGACTGTGCCTGTTCTCCCTCGCAGCTGA | |
| 2B 2321 | ACTATTGTTGAAGTATGACATACATTCAGAAACCTGTGCAATGTATGTGTACGATTGGTGTCTTTTATGGAGCTAA | |
| 2C 2401 | E L H C E A L R G S P L I L Y R F H E D V T L G N | 795 |
| 2A 2401 | TGGAGCTTCACTGTAGGCCCTGAGAGGCTCTCCCTGTATCTCTGATCCTGTACCGGTTTTTTTCATGAGGATGTCAACCTAGGAGCT | |
| 2B 2401 | AAATGGAGCCACAGAGCTCTCAGGGCTGTTGGTGTGTGGCAATCCAGCACACTTCTCCTGCCTGCAGAACCTCCCTGTG | |
| 2B 2401 | GTTCCTCTGTTTTTACTTGAATCTTTGTTTATAGAAACTGGGGAAAGTTTACTTTCTTTTCAGAGAAAGCCAAATGGTA | |
| 2C 2481 | R S S P S G G A S L N L S L T A E H S G V Y S C E A D | 822 |
| 2A 2481 | AGGTGCTCCCTCTGAGGAGCGTCTTAACTCTCTCTGACTGCAGAGCACTCTGGAACCTCTCTCTGTGAGGCCGA | |
| 2B 2481 | AAAGTCTCGATCCTTTGTGTPATGTTTCCAGGAATCTGATGTTTCCAGCAGCTCTTTCTTGAAGATGATCAAGACACCTC | |
| 2B 2481 | TGATAGAAAAATCTTGAGCCTGATGTGTCAGACATGCCCCCTAGCAATACTTGTGAGTAAAGAGGTTATTTTAAAAATGT | |
| 2C 2561 | N G L G A Q R S E T V T L Y I T G L T A N F S G P F A | 849 |
| 2A 2561 | CAATGGCTCGGGGCCCCAGCAGTGAGACAGTACACTTTATATCAGGGCTGACCGGAAACAGAGTGGCCCTTTTG | |
| 2B 2561 | ACTAAATGCAATAAGACTTTTTTAGAACATAAATACTATATCTTGAACCTGAAATTTATACATGAAAAATGAACCAAGA | |
| 2B 2561 | GAATGTTCTGAGACTACTCCAAGTCAGAGCCAAATCTACTAGGAAGCTTCTAGACITTCACCTCATTTCTGCATCCCATAC | |
| 2C 2641 | T G V A G G L L S I A G L A A G A L L L Y C W L S R | 875 |
| 2A 2641 | CCACAGAGTCCGGGGCTGCTCAGCATAGCAGGCCCTTGTCTGGGGGCACCTGTGCTCTACTGTGGCTCTCGAGA | |
| 2B 2641 | ATTCTGAGCATATGTTTCTCTGCGGTAGAAAGATTAAGCTGTTTCTGTCCGGAATCTCTCTCATTTGACTTCTTAAGAA | |
| 2B 2641 | TATCTTTTATCCATGTTTTTACTTTCTCTCATATTCAGCAGCATCTTAAGCCTCTTTTATTTTCTGTCTTCTGACTGTCA | |
| 2C 2721 | K A G R K P A S D P A R S P S D S D S Q E P T Y H N N X | 902 |
| 2A 2721 | AAAGCAGGAGAAAGCCTGCTCTGACCCCGCAGGAGCCCTTCAGACTCGGACTCCCAAGAGCCCCACCTATCACAATGT | |
| 2B 2721 | GCCTCTACTTGTAGTCTCTTTCATTACTGGGAGTAAATGTTCTTCACTATTTCCACATTAATAATCCTATGTTAACGA | |
| 2B 2721 | CCCTTAATGCCAGTAGAATGTAAGCTTTCATGAGAACAGAACTGCATCCATCTTGGTCTTTCACAACATCCCTCTGCTGCTACT | |

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FIGURE 18B-2A

| | | | |
|----|------|---|-----|
| 2C | 2801 | P A W E E L Q P V Y T N A N P R G E N V V Y S E V R I | 929 |
| 2A | 2801 | ACCAGCCTGGGAAGAGCTGCAACACAGTGTAACATAATGCAATCCTAGAGGAGAAATGTGGTTTACTCAGAAAGTACGGA | |
| 2B | 2801 | AAAAA | |
| | 2801 | CAGTGTGGGCACACAGTAGGTCTCTCAGTCAACATTTGTAAATTTAGTGGACAGATGATATGACAAGATGATAAGAGGGGA | |
| 2C | 2881 | I Q E K K K H A V A S D P R H L R N K G S P I I Y S | 955 |
| 2B | 2881 | TCATCCAAAGAGAAAAAAGAAACATGCAGTGGCCTCTGACCCAGGCATCTCAGGAACCAAGGGTTCCCTTATCATCTACTCT | |
| | 2881 | TTTTAAAAAATCATCTAGCAAGCCCAAGAGGAAAAAACAAGCTATTTTAGAAATGAAATACCAATTTGAAGCAGTA | |
| 2C | 2961 | E V K V A S T P V S G S L F L A S S A P H R * stop | 977 |
| 2B | 2961 | GAAGTTAAGGTGGCGTCAACCCCGGTTTCCGGATCCCTGTTCTTGGCTTCTCAGCTCCTCACAGATGAGTCCACACAGTC | |
| | 2961 | AGAATAGATTGGATATCTTTGAAAACCATTAATTGAATGAAGAACCAATTTGAGAAACAATACAGAAATGCACAAAGTAGAA | |
| 2C | 3041 | TCCTCAACTGCTGTTTCAGCCTCTGCACCCCAAGTTCCCTTTGGGGGAGAGCAGCATTTGAAGTGGGAAGATTTAGGCT | |
| 2B | 3041 | AGATACAGAAATTAAGGCAAAAGTTATAATATGAAATCAGACAATGGATTTGTCTGTATCCAGTTATCTGGATAATTA | |
| 2C | 3121 | GCCCCAGACCATATCTACTGGCCTTTGTTTTCACATGTCCTCAATTCAGTCTGACCAGAATGCAGGGCCCTGCTGGACTG | |
| 2B | 3121 | AATGGAGACCCTCAGAAAAATTGAACCGAAGAGTAAATGAACTCAAAATGTAGTAAAGAAATTTGTTGGAAAGTAAAGAAA | |
| 2C | 3201 | TCACCTGTTTCCAGTTAAAGCCCTGACTGGCAGGTTTTTTTAAATCCAGTGGCAAGGTGCTCCCACTCCAGGGCCCCAGCAC | |
| 2B | 3201 | ACTTGAATATGTAGATCAGAACATATATGTTGATGACGTTATGACTTTGAGGTTAAAAATATATATATGTGCTCCCTATGAT | |
| 2C | 3281 | ATCTCCTGGATTCCCTTAGTGGGCTTCAGCTGTGGTTGCTGTTCTGAGTACTGCTCTCATCACACCCCCACAGAGGGGGTC | |
| 2B | 3281 | TATGGGAAAAAAGCAGTCGTCTCAGAAAGAAAAACATCAAGTTAGTCTTAGACTTTGCACTGCACTCAGTACCAAGAG | |
| | 3361 | TTACCACACAAAGGAGAGTGGCCCTTCAGGAGATGCCGGTGGCCCTAACAGCTCAGGTGCTCCTAACTCCGACACAG | |
| | 3441 | AGTTCTCTGCTTTGGGTGGATGCATTTCTCAATTGTCTCATAGCTGGTGGGCTACTGCACTGTGTGCTGCAAAATGGGACAG | |
| | 3521 | CACACAGCCTGTGCACATGGGACATGTGATGGGTCTCCCCACGGGGCTGCATTTTACACTCTCTCCACTCTGTCTCAAACT | |
| | 3601 | CTAAGGTGGCCTGTGACACCAAGTAACTTCTCTCTGCTCATGTGCTAGTGTCTACCTGCCCCAAGTAAAGTGGCTTCA | |
| | 3681 | TACACCAAGTCCCGAAGTCTTCCCATCTTAACAGAAAGTAAACCCAGCAAGTCAAGCCAGGAGGACCAGGGGTGCAGACA | |
| | 3761 | GAACACATACCTGGAACACAGGAGGTGCTCAATTAATTTGACTGACTGACTGAATGAATGAATGAATGAAGAAAGAAAC | |
| | 3841 | TGTGGTAAATCAAACTGGCATAAAAATCCAGTCACTCCCTAGGAAATCCGGGAGGTATTTCTGGCTTCTTAAGAAACAACG | |
| | 3921 | GAAGAGAGGAGCTTGGATGAAGAAACTGTTGAGCAAGAGAGGGCTTCTTTCACACTTTTATGTGCTTGTGGATCACCT | |
| | 4001 | GAGGATCTGTGAAAAATACAGATACCTGATTTCAGTGGGTCTGTGTGAGAGCCCTGAGACTGCCATTCTTAACATGTTCTCCAGGGG | |

FIGURE 18B-3

4081 ATGCTGATGCTGCTGGCCCTGGGACTGCACTGCATGCACTGTGAAGCCCTATAGGTCTCAGCAGAGGCCCATGGAGAGGA
 4161 ATGTGTGGCTCTGGCTGCCAGGGCCCAACTCGGTTACACGGATCGTGTCTCCTGGCCAGCCCTTTGGCCACAGCAC
 4241 CACCAGCTGCTGTTGCTGAGAGAGCTTCTTCTGTGACATGTTGGCTTTTCATCAGCCACCCCTGGGAAGCGAAAGTAGC
 4321 TGCCACTATCTTTGTTTCCCACTCAGGCCCTCACACTTTCCCATGAAGGGTGAATGATATTAACCTGAGCCCTCTCC
 4401 ATTCAGAGTTGTTCTCCCATCTCTGAGCAATGGGATGTTCTGTTCCGCTTTTATGATATCCATCACATCTTATCTTGATC
 4481 TTTGCTCCAGTGGATTGTACAGTGTGACTTTTAAGCCCCACGGCCCTGAAATAAATCCTTCCAAGGCAATTGGAAGC
 4561 TCACCTCACCTGAACCATGGCTTTTCATGCTTCCAAAGTGTACAGGCCCTTGCCCAAGATAGACAGGGCTGACTCTGCTGCCC
 4641 CAACCTTCAAGGAGGAACCCAGACACCTGAGACAGGAGCCTGTATGAGCCCCAGTGCAGCCTTGCGAGGACACAGGCTG
 4721 GAGGCATTTGTCATCACTACAGATATGCAACTAAATAGACGTGGAGCAAGAGAAATGCATTTCCACCGAGGCCGCTTTT
 4801 TTAGGCCCTAGTTGAAAGTCAAGAGGACAGCAGCAAGCATAGGCTCAGGATTAAGAAAAAATCTGCTCACAGTCTGTT
 4881 CTGGAGGTCACATCACCAACAAGCTCACGCCCTATGCAGTTCTGAGAAGGTGGAGGCCACCCAGGCTCAAAAGAGGAAAT
 4961 TAGAATTTCTCATTTGGGAGAGTAAGGTACCCCATCCAGATGATACTGCACAGTGGCAGAACAACTCCACCCCTAAT
 5041 GTGGTGGACCCCATCCAGTCTGTTGAAGCCTGAATGTAAACAAAGGGCTTATCTTCTCAAGTAAGGGGGAACCTCCT
 5121 GCTTTGGGCTGGGACATAAGTTTCTGCTTTCAGACCGCAACTGAAAAATGGCTCTTCTTGGGTCTTGAGCTTGCTGGC
 5201 ATATGGACTGAAAGAACTATGCTATTTGGATCTCCTGGATCTCCAGCTTGCTGACTGCAGATCTTGAGATATGTACGCT
 5281 CTACAGTCACAAGAGCTAATTCATTCTAATAAACCAATCTTTTC

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FIGURE 18C-1

1 AGTGAAGGGGTTCCCATATGAAAAATACAGAAGAATTATTGAATACTA
52 GCAATACACAACCTTGATATTTCTAGAGAACCCAGGCACAGTCTTGGAGAC
103 ATTACTCTGAGAGACTGCAGCTGATGGAAGATGAGCCCCCACTTCTAAAA
154 ATGTATCACTACCGGATTGAGATACAAACAGCATTTAGGAAGTCTCATC
205 TGAGTAGCAGCTTCTGCGCTCTTCTTGGAGATAAGTCGGGCTTTTGGTG
256 AGACAGACTTTCCCAACCCCTCTGCGCGCGTGCCTTCTCTGTGGCT
1 M L L W L
307 GCTGCTGTGATCTCTGATCTGGAAGAGAACAAATCAGGGTGGCCCCAAA
6 L L L I L T P G R E Q S G V A P K
358 AGCTGTACTTCTCTCAATCTCCATGGTCCACAGCCTTCAAAGGAGAAAA
23 A V L L L N P P W S T A F K G E K
409 AGTGGCTCTCATATGCAGCAGCATATCACATTCCTTAGCCAGGAGACAC
40 V A L I C S S I S H S L A Q G D T
460 ATATTGGTATCACGATGAGAAGTTGTTGAAAAATAAACATGACAAGATCCA
57 Y W Y H D E K L L K I K H D K I Q
511 AATTACAGAGCCTGGAATTTACCAATGTAAAGCCCGAGGATCCTCCCTCAG
74 I T E P G N Y Q C K T R G S S L S
562 TGATGCCGTGCATGTGGAATTTTCACCTGACTGGCTGATCCTGCAGGCTTT
91 D A V H V E F S P D W L I L Q A L
613 ACATCTGTCTTTGAAGGAGACAAATGTCAATCTGAGATGTCAGGGGAAAGA
108 H P V F E G D N V I L R C Q G K D
664 CAACAAAAACACTCATCAAAAGTTTACTACAAGGATGGAAAACAGCTTCC
125 N K N T H Q K V Y Y K D G K Q L P
715 TAATAGTTATAATTTAGAGAAGATCACAGTGAATTCAGTCTCCAGGGATAA
142 N S Y N L E K I T V N S V S R D N
766 TAGCAATATCATTTGACTGCTTATAGGAAGTTTACATACATTGACATTGA
159 S K Y H C T A Y R K F Y I L D I E
817 AGTAACTTCAAAACCCCTAAATATCCAAGTTCAAGAGCTGTTTCTACATCC
176 V T S K P L N I Q V Q E L F L H P
868 TGTGCTGAGAGCCAGCTTCTCCACGCCCATAGAGGGGAGTCCCATGACCCCT
193 V L R A S S S T P I E G S P M T L
919 GACCTGTGAGACCCAGCTCTCTCCACAGAGCCAGATGTCCAGCTGCAATT
210 T C E T Q L S P Q R P D V Q L Q F
970 CTCCTCTTTCAGAGATAGCCAGACCCCTCGGATTGGGCTGGAGCAGGTCCCC
227 S L F R D S Q T L G L G W S R S P

FIGURE 18C-1A

1021 CAGACTCCAGATCCCTGCCATGTGGACTGAAGACTCAGGGTCTTACTGGTG
244 R L Q I P A M W T E D S G S Y W C
1072 TGAGGTGGAGACAGTCACTCACAGCATCAAAAAAGAGCCTGAGATCTCA
261 E V E T V T H S I K K R S L R S Q
1123 GATACGTGTACAGAGATCCCTGTGTCTAATGTGAATAGAGATCCGGCC
278 I R V Q R V P V S N V N L E I R P
1174 CACCGAGGGCAGCTGATTGAAGGAGAAAAATATGTCCTTATTGCTCAGT
295 T G G Q L I E G E N M V L I C S V
1225 AGCCCAGGGTTCAGGGACTGTCACATTCCTCGCACAAAGAAAGAGAGT
312 A Q G S G T V T F S W H K E G R V
1276 AAGAAGCCTGGGTAGAAAGACCCAGCGTCCCTGTTGGCAGAGCTGCATGT
329 R S L G R K T Q R S L L A E L H V
1327 TCTCACCGTGAAGGAGAGTGATGCAGGGAGATACTACTGTGCAGCTGATAA
346 L T V K E S D A G R Y Y C A A D N
1378 CGTTCACAGCCCCATCCTCAGCACGTCGGATTCGAGTCACCGTGAGATTCC
363 V H S P I L S T W I R V T V R I P
1429 GGTATCTCACCCCTGCTCCCTCACCTTCAGGGCTCCAGGGCCACACTGTGCT
380 V S H P V L T F R A P R A H T V V
1480 GGGGGACCTGTGGAGCTTCACTGTGAGTCCCTGAGAGCTCTCCCCCGAT
397 G D L L E L H C E S L R G S P I
1531 CCTGTACCGATTTATCATGAGGATGTCAACCTGGGGAACAGCTCAGCCCC
414 L Y R F Y H E D V T L G N S A P
1582 CTCTGGAGGAGGAGCCTCCTTCAACCTCTCTCTGACTGCAGAACATCTGG
431 S G G G A S F N L S L T A E H S G
1633 AAACCTACTCCTGTGATGCAGACAATGGCCCTGGGGGCCAGCACAGTCATGG
448 N Y S C D A D N G L G A Q H S H G
1684 AGTGAGTCTCAGGGTCACAGTTCGGGTGTCTCGCCCTCCTCACCCCTCAG
465 V S L R V T V P V S R P V L T L R
1735 GGCTCCGGGGCCAGGCTGTGTGGGGGACCTGTGGAGCTTCACTGTGA
483 A P G A Q A V V G D L L E L H C E
1786 GTCCCTGAGAGGCTCCTTCCCGATCCTGTACTGGTTTATCACGAGGATGA
499 S L R G S F P I L Y W F Y H E D D
1837 CACCTTGGGGAACATCTCGGCCCACTCTGGAGGAGGGGCATCCTTCAACCT
516 T L G N I S A H S G G A S F N L
1888 CTCTCTGACTACAGAACATTTCTGGAACACTACTCATGTGAGGCTGACAAATGG
533 S L T T E H S G N Y S C E A D N G

FIGURE 18C-2

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FIGURE 18D-1

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1 TGGTGACCAAGAGTACATCTCTTTTCAAATAGCTGGATTAGTCTCCTCATGC
1 M L
52 TGCTGTGGTCATTTGCTGTCATCTTTTGATGCAGTCACTGAACAGGCAGATT
19 L W S L L V I F D A V T E Q A D S
103 CGCTGACCCCTTGTGGCCCTCTTCTGTCTTCGAAGGAGACAGCATCGTTC
36 L T L V A P S S V F E G D S I V L
154 TGAATGCCAGGGAGAACAGAACTGGAAATTCAGAAGATGGCTTACCATA
53 K C Q G E Q N W K I Q K M A Y H K
205 AGGATAACAAGAGTTATCTGTTTCAAAAAATCTCAGATTTCCTTATCC
70 D N K E L S V F K K F S D F L I Q
256 AAAGTGCAGTTTAAAGTGACAGTGGTAACTATTCTGTAGTACCAAGGAC
87 S A V L S D S G N Y F C S T K G Q
307 AACTCTTCTCTGGGATAAACTTCAAATATAGTAAAGATAAAAGTCCAAG
104 L F L W D K T S N I V K I K V Q E
358 AGCTCTTCAACGTCCTGTGCTGACTGCCAGCTCCTTCCAGCCCATCGAAG
121 L F Q R P V L T A S S F Q P I E G
409 GGGTCCAGTGAGCCTGAATGTGAGACCCGGCTCTCTCCACAGAGGTGG
138 G P V S L K C E T R L S P Q R L D
460 ATGTTCAACTCCAGTTCTGCTTCTTCAGAGAAACACAGGTCTGGGTGAG
155 V Q L Q F C F F R E N Q V L G S G
511 GCTGGACAGCTCCGGAGCTCCAGATTTCGCCGTGTGGAGTGAAGACA
172 W S S S P E L Q I S A V W S E D T
562 CAGGTCTTACTGGTCAAGGCAGAAACGGTGACTCACAGGATCAGAAAC
189 G S Y W C K A E T V T H R I R K Q
613 AGAGCTCCAATCCAGATTACGTGCAGAGATCCCCATCTCTAATGTAA
206 S L Q S Q I H V Q R I P I S N V S
664 GCTTGGAGATCCGGCCCCCGGGGACAGGTGACTGAAGGACAAAACTGA
223 L E I R A P G G Q V T E G Q K L I
715 TCCTGTCTGTCTAGTGGCTGGGGGTACAGGAAATGTACATTTCTCCTGGT
240 L L C S V A G G T G N V T F S W Y
766 ACAGAGAGCCACAGGAACCATGTATGGGAAGAAACCCAGCGTTCCTGT
257 R E A T G T S M G K K T Q R S L S
817 CAGCAGAGCTGGAGATCCAGCTGTGAAGAGAGTGTATCCCGCAATATT
274 A E L E I P A V K E S D A G K Y Y
868 ACTGTAGAGCTGACACGGCCATGTGCCTATCCAGAGCAAGGTGTGAATA
291 C R A D N G H V P I Q S K V V N I
919 TCCCTGTGAGAAATCCAGTGTCTCGCCCTGTCTCACCCTCAGGTCTCTG
308 P V R I P V S R P V L T L R S P G
970 GGGCCAGGTGAGTGGGACCTGTGGAGCTTCACTGTGAGGCCCTGA
325 A Q A A V G D L L E L H C E A L R
1021 GAGGCTCTCCCCCAATCTTGTACCAATTTTATCATGAGGATGTCACCCCTG
342 G S P P I L Y Q F Y H E D V T L G
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FIGURE 18D-1A

1072 GGAACAGCTCGGCCCTCTGTGAGGAGGGGCTCCTTCAACCTCTCTTTGA
359 N S S A P S G G A S F N L S L T
1123 CTGCAGAACATTCTGGAACTACTCCTGTGAGGCCAACACGGCTGGGG
376 A E H S G N Y S C E A N N G L G A
1174 CCCAGTGCAGTGGCAGTCCAGTCTCCATCTCAGGACCTGATGGCTATA
393 Q C S E A V P V S I S G P D G Y R
1225 GAAGAGACCTCATGACAGTGGAGTTCTCTGGGACTGTTGGTGTCTCTG
410 R D L M T A G V L W G L F G V L G
1276 GTTTCACCTGGTGTGCTGTGCTATGCCCTTCTCCACAAGATATCAG
427 F T G V A L L L Y A L F H K I S G
1327 GAGAAAGTTCTGCCACTAATGAACCCAGAGGGCTTCCAGGCCAAATCCTC
444 E S S A T N E P R G A S R P N P Q
1378 AAGAGTTCACCTATTCAAGCCCAACCCAGACATGGAGGAGCTGCAGCCAG
461 E F T Y S S P T P D M E E L Q P V
1429 TGTATGTCATGTGGGCTCTGTAGATGGATGGTGTATTTCTCAGGTCT
478 Y V N V G S V D V D V V Y S Q V W
1480 GGAGCATGCAGCAGCCAGAAAGCTCAGCAACATCAGGACACTTCTGGAGA
495 S M Q Q P E S S A N I R T L L E N
1531 ACAAGGACTCCCAAGTCATCTACTTCTGTGAAGAAATCATACACTTGG
512 K D S Q V I Y S S V K K S
1582 AGGAATCAGAAGGGAGATCAACAGCAAGGATGGGGCATCATTAAGACTTG
1633 CTATAAAACCTTATGAAAATGCTTGAGGCTTATCACCTGCCACAGCCAGAA
1684 CGTGCTCAGGAGGCACCTCCTGTCTATTTTCTCCTGATGATGTTCTTCT
1735 CCAATATCTTTTACCTATCAATATTCAATTGAACCTGCTGTACATCCAG
1786 ACACGTGCAAAATAATTATTTCTGTACCTTCTTTAAGCAATCAGTGTG
1837 TAAAGATTTGAGGGAAGAATGAATAAGAGATACAAAGGTCTCACCTTCATCT
1888 ACTGTGAAGTGTAGAGAACAGGACTTGATAGTGGTGTATTAACCTTATTTAT
1939 GTGCTGTGGATACAGTTTGTCTAATAATTTTGTGTGAGAAATTTTGGCAATAT

FIGURE 18D-2

1990 GTTCATTGGGAATATTGGCCCTGAAATTTTCTTTCCACTGTGTCTCTGCCA
2041 GAATGTTTGTATCAGGCTGATGCTGGCTTCATAGAATGAGTTAGGCAGGAG
2092 CCCTTCCTCCTTGATTTTGGCATAGTTTCAGCAGGATTTGGTACCAGTTA
2143 TTCTTTCTGCATCTGTAGAAATTCAGCTATGAATCCATCTGGTCTAGGCT
2194 TTTGTGTTGGTTGGTAAGTTTTTTTATTACTAATTCAACTTCAGCGCTTGAT
2245 ATTGGTCTAGGAGGGTTTCTCTCTCTCCCTGGTTCAATCTTGGGAGATTG
2296 TGTGTTTCCAGGAATTTAGCCGTTTCTCCAGATTTTCTCTTTATGTGCA
2347 TCGACTTGAGTGAACATACATATATATGCACCTGGGAAACCAAAAACTCTG
2398 TGTGACTTGCTTTATTTGCAGCATTTGTTTTTATTTTGGTAGTCTGGAAGTGA
2449 ACCTGCAATATCACCAAGTATGCATATAGTTGCAAAAAATGTGATTTTTTGA
2500 CATAGTAAATATGAGTATTTGCAATAAACATATGATATTACITTTTGTAAAGTA
2551 TATAGATAAAAAATGTAAATAATCTATATAAA

58/60

FIGURE 18E-1

1 GAGGCATCTCTAGGTACCATCCCTGACCTGGTCCTC
37 ATGCTGCCGAGGCTGTGCTGTGATCTGTGCTCCACTCTGTGAA
M L P R L L L I C A P L C E
82 CCTGCCGAGCTGTTTTGATAGCCAGCCCTCCCATCCACAGAG
P A E L F L I A S P S H P T E
127 GGGAGCCCGAGTGACCCCTGACGTGTAAGATGCCCTTTCTACAGAT
G S P V T L T C K M P F L Q S
172 TCAGATGCCCCAGTCCAGTTCTGCTTTTTCAGAGACACCCGGGCC
S D A Q F Q F C F F R D T R A
217 TTGGGCCCCAGGCTGGAGCAGCTCCCCCAAGCTCCAGATCGCTGCC
L G P G W S S S P K L Q I A A
262 ATGTGGAAGAAGACACAGGCTCATCTGTGCGAGGCACAGACA
M W K E D T G S Y W C E A Q T
307 ATGGCGTCCAAAGTCTTGAGGAGCAGGAGATCCCAGATAAATGTG
M A S K V L R S R R S Q I N V
352 CACAGGGTCCCTGCTGCTGATGTGAGCTTGAGAGACTCAGCCCCCA
H R V P V A D V S L E T Q P P
397 GGAGGACAGGTGATGGAGGAGACAGGCTGGTCTCATCTGCTCA
G G Q V M E G D R L V L I C S
442 GTTGCTATGGGCACAGGAGACATCACCTTCCTTTGGTACAAAGGG
V A M G T G D I T F L W Y K G
487 GCTGTAGGTTAAACCTTCAGTCAAGACCCAGCGTTCACTGACA
A V G L N L Q S K T Q R S L T
532 GCAGAGTATGAGATTCCTCAGTGAGGAGAGTGATGCTGAGCAA
A E Y E I P S V R E S D A E Q
577 TATTACTGTGTAGCTGAAATGGCTATGGTCCCAGCCCCAGTGGG
Y Y C V A E N G Y G P S P S G
622 CTGGTGAGCATCACTGTCAGAATCCCGGTGTCTCGCCCCAATCCTC
L V S I T V R I P V S R P I L
667 ATGCTCAGGCTCCAGGCCAGGCTGCAGTGGAGGATGTGCTG
M L R A P R A Q A A V E D V L
712 GAGCTTCACTGTAGGCCCTGAGAGGCTCTCCTCCAAATCCTGTAC
E L H C E A L R G S P P I L Y
757 TGGTTTTATCAGGAGGATATCACCTTGGGAGCAGGTGCGGCCCCC
W F Y H E D I T L G S R S A P
802 TCTGGAGGAGGAGCCTCCTTCAACCTTCCCTGACTGAAGAACAT
S G G G A S F N L S L T E H
847 TCTGGAACCTACTCTGTGAGGCCAACAATGGCCTGGGGGGCCAG
S G N Y S C E A N N G L G A Q
892 CGCAGTGAGGCGGTGACACTCAACTTCACAGTGCCTACTGGGGCC
R S E A V T L N F T V P T G A

FIGURE 18E-1A

937 AGAAGCAATCATCTTACCTCAGGAGTCATTGAGGGGCTGCTCAGC
R S N H L T S G V I E G L L S
982 ACCCTTGGTCCAGCCACCGTGGCTTATTATTGCTACGGCCTC
T L G P A T V A L L F C Y G L
1027 AAAAGAAAAATAGGAAGACGTTTCAGCCAGGGATCCACTCAGGAGC
K R K I G R R S A R D P L R S
1072 CTTCCAGCCCTTACCCCAAGAGTTCACCTACCTCAACTCACCT
L P S P L P Q E F T Y L N S P
1117 ACCCAGGGCAGCTACAGCCTATATATGAAATGTGAATGTGTGA
T P G Q L Q P I Y E N V N V V
1162 AGTGGGATGAGTTTATTCTACTGGCGTACTATATAACCCGCGGAG
S G D E V Y S L A Y N Q P E
1207 CAGGAATCAGTAGCAGCAGAAACCCCTGGGACACATATGGAGGAC
Q E S V A A E T L G T H M E D
1252 AAGTTTCCCTTAGACATCTATTCCAGGCTGAGGAAAGCAACATT
K V S L D I Y S R L R K A N I
1297 ACAGATGTGGACTATGAAGATGCTATGTAA 1326
T D V D Y E D A M *
GGTT ATGGAAGATT CTGCTCTTTG
1351 AAAACCATCC ATGACCCCAA GCCTCAGGCC TGATATGTTT TTCAGAGATC
1401 CTGGGGCATT AGCTTTCCAG TATACCTCTT CTGGATGCCA TTCTCCATGG
1451 CACTATTCTT TCATCTACTG TGAAGTGAAG TTGGCGCAGC CCTGAAGAAA
1501 CTACCTAGGA GAACTAATAG ACACAGGAGT GACAGGACT TTGTTATCAG
1551 AACCAGATTC CTGCCGGCTC CTTTGAAAC AGGTCAATTT GTGCTCTTCT
1601 GTTTACAAGA GGAACAAGA TGGAAATAAA GAAATTGGGA TCCTGGGTTG
1651 GAGGACAGT GAAGCTTAGA GCACATGAAC TCAAGGTTAG TGACTCTGCA
1701 GGACTTCACA GAGAGAGCTG TGCCCATCAT TCAGTCCAAG TGCTTTCTCT
1751 GCCCAGACAG CACAGAATC CAGCCCGCT ACCTACATGG ATCATCGAGT
1801 TTCCACCTAA AATATGATTC TATTTATTTT GAGTCACTGT TACCAAAATTA

FIGURE 18E-2

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1851 GAACTAAAC AAAGTTACAT AAAAAGTTAT TGTGACTCCA CTTAATTTTA
1901 GTGACGTATT TTTGTATATA TAGGCAACC TATACCACAT CCAAAATTAT
1951 GTATCTATTA CAGCCCCTAG AAGCTTTATA AATACAGTGT GTCTTCTTTT
2001 ATTCACAAA TTTTGAAT CGTGGTAATA TGGTTGAAA CCTGTATCTT
2051 AATTATTTT TTTTAAAT GAGACAGGT CTCACTCTGT CACTCAATCT
2101 GGAATGCAGT GGCACAATCT TGCCTCACTG CAACGCTGC CTCTCAGGCT
2151 CAAGCAAACC TCTCACCTCA GCCTGCTGAG TAGCTGGGAC TACAGGCACA
2201 TGCCACCAAA CTGGGCCATT TTTTGTCTTA CGTAGAGACA AGATTTCAAC
2251 GTTTTGCCCA GGCTGGTCTC AAATCCTCTG GCTCAAGCAA TGTATTGAAT
2301 TTT
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